



SEQUENCE LISTING

<110> Edinger, Shlomit R
Gerlach, Valerie
MacDougall, John R
Malyankar, Muriel M
Smithson, Glennnda
Millet, Isabelle
Peyman, John A
Stone, David J
Gunther, Erik
Ellerman, Karen
Shimkets, Richard A
Padigaru, Muralidhara
Guo, Xiaojia
Patturajan, Meera
Taupier Jr, Raymond J
Burgess, Catherine E
Zerhusen, Bryan D
Kekuda, Ramesh
Spytek, Kimberly A
Gangolli, Esha A
Fernandes, Elma R
Gorman, Linda

<120> Proteins and Nucleic Acids Encoding Same

<130> 21402-168

<140> 09/981,151
<141> 2001-10-16

<150> 60/241,040
<151> 2000-10-17

<150> 60/241,058
<151> 2000-10-17

<150> 60/241,063
<151> 2000-10-17

<150> 60/241,243
<151> 2000-10-17

<150> 60/242,152
<151> 2000-10-20

<150> 60/242,482
<151> 2000-10-23

<150> 60/242,611
<151> 2000-10-23

<150> 60/242,612
<151> 2000-10-23

<150> 60/242,880

<151> 2000-10-24

<150> 60/242,881

<151> 2000-10-24

<150> 60/259,028

<151> 2000-12-29

<150> 60/269,813

<151> 2001-02-20

<150> 60/286,324

<151> 2001-04-25

<150> 60/294,108

<151> 2001-05-29

<150> 60/303,968

<151> 2001-07-09

<160> 160

<170> PatentIn Ver. 2.1

<210> 1

<211> 2997

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (857)..(858)

<223> Wherein n is an a or t or c or g.

<220>

<221> misc_feature

<222> (2383)

<223> Wherein n is an a or t or c or g.

<220>

<221> misc_feature

<222> (2983)

<223> wherein n is an a or t or c or g.

<400> 1

```
cgctcctgga tgaagccccg cgcgcgcgga tggcggggct tggcggcgct gtggatgctg 60
ttggcgcagg tggccgagca ggtgagtccc gggcgctccc accagcgcgg aaaccgcggg 120
tccggacagc tggaggcgag tccccgcggg ctcctctccc gcggaccccc cgtctccacc 180
gcgatgtcgc cgctgttttc cgcaggcacc tgcgtgcgcc atgggacccg cagcggcagc 240
gcctgggagc ccgagcgtcc cgcgtcctcc tccaccgcgg gagcggcccg gctggatgga 300
aaagggcggg acatggatga agctggaaac catcgttttc agcaaactaa cacaggaaca 360
gaaaaccaa cactgcatgt tctcactcaa tatgacctgg tctctgccta cgaggttgac 420
cacaggggag attacgtgtc ccatgaaatc atgcaccatc agcggcggag aagagcagtg 480
gccgtgtccg aggttgagtc tcttcacctt cggctgaaag gccccaggca cgacttccac 540
atggatctga ggacttccag cagcctagtg gctcctggct ttattgtgca gacgttggga 600
aagacaggca ctaagtctgt gcagacttta ccgccagagg acttctgttt ctatcaaggc 660
tctttgcgat cacacagaaa ctcgccatcg catggaggga agttctgtga gggctccact 720
```

cgactctga	agctctgcaa	cagtcagaaa	tgtccccggg	acagtgttga	cttccgtgct	780
gctcagtg	ccgagcacia	cagcagacga	ttcagagggc	ggcactacaa	gtggaagcct	840
tacactcaag	tagaagnnga	cttatgcaaa	ctctactgta	tgcagaagg	atttgatttc	900
ttcttttctt	tgtcaaataa	agtcaaagat	gggactccat	gctcggagga	tagccgtaat	960
gtttgtatag	atgggatatg	tgagctcagt	gtgggtgtcca	catctgcgca	catgccccag	1020
cctcccaagg	aagacctctt	catcttgcca	gatgagtata	agtcttgctt	acggcataag	1080
cgctctcttc	tgaggtccca	tagaaatgaa	gaactgaacg	tggagacctt	ggtggtggtc	1140
gacaaaaaga	tgatgcaaaa	ccatggccat	gaaaatatca	ccacctacgt	gctcacgata	1200
ctcaacatgg	tatctgcttt	attcaaagat	ggaacaatag	gaggaaacat	caacattgca	1260
attgtaggtc	tgattcttct	agaagatgaa	cagccaggac	tggtgataag	tcaccacgca	1320
gaccacacct	taagtagctt	ctgccagtgg	cagtctggat	tgatggggaa	agatgggact	1380
cgctcatgacc	acgccatctt	actgactggg	ctggatatat	gttcctggaa	gaatgagccc	1440
tgtgacactt	tgggatttgc	accataagt	ggaatgtgta	gtaaatatcg	cagctgcacg	1500
attaatgaag	atacaggtct	tggactggcc	ttcaccattg	cccatgagtc	tggacacaac	1560
tttggcatga	ttcatgatgg	agaagggaac	atgtgtaaaa	agtccgaggg	caacatcatg	1620
tcccctacat	tggcaggacg	caatggagtc	ttctcctggg	cacctgcag	ccgccagtat	1680
ctacacaaat	ttctaagcac	cgctcaagct	atctgccttg	ctgatcagcc	aaagcctgtg	1740
aaggaatata	agtatcctga	gaaattgcc	ggagaattat	atgatgcaaa	cacacagtgc	1800
aagtggcagt	tcggagagaa	agccaagctc	tgcatgctgg	actttaaaaa	ggacatctgt	1860
aaagccctgt	ggtgccatcg	tattggaagg	aaatgtgaga	ctaaatttat	gccagcagca	1920
gaaggcacia	tttgtgggca	tgacatgtgg	tgccggggag	gacagtgtgt	gaaatatggt	1980
gatgaaggcc	ccaagcccac	ccatggccac	tggtcggact	ggtcttcttg	gtcccatg	2040
tccaggacct	gcggaggggg	agtatctcat	aggagtcgcc	tctgcaccaa	ccccaatcca	2100
tcgcatggag	ggaagttctg	tgagggctcc	actcgcactc	tgaagctctg	caacagtcag	2160
aaatgtcccc	gggacagtgt	tgacttccgt	gctgctcagt	gtgccgagca	caacagcaga	2220
cgattcagag	ggcggcacta	caagtggaag	cctcaggact	tatgcaaact	ctactgtatc	2280
gcagaaggat	ttgatttctt	cttttctttg	tcaaataaag	tcaaagatgg	gactccatgc	2340
tcggaggata	gccgtaaatg	ttgtatagat	gggatagtgt	agnttgatg	tgacaatgtc	2400
cttggatctg	atgctgttga	agacgtctgt	ggggtgtgta	acgggaataa	ctcagcctgc	2460
acgattcaca	ggggtctcta	caccaagcac	caccacacca	accattatca	catggtcacc	2520
attccttctg	gagcccgagg	tatccgcata	tatgaaatga	acgtctctac	ctcctacatt	2580
tctgtgcgca	atgccctcag	aaggtactac	ctgaatgggc	actggaccgt	ggactggccc	2640
ggccggtaca	aattttcggg	cactactttc	gactacagac	ggtcctataa	tgagcccag	2700
aacttaatcg	ctactggacc	aaccaacgag	acactgattg	tggagctgct	gtttcaggga	2760
aggaaccg	gtgttgctg	ggaatactcc	atgcctcgct	tggggaccga	gaagcagccc	2820
cctgccagc	ccagctacac	ttgggccatc	gtgcgctctg	agtgtccgt	gtcctgcgga	2880
gggggtagg	gccttcag	gctgctcctg	gaggcagcat	gtcagccttc	agccactgcg	2940
tacattgcac	tggcctttct	tgaatcctaa	tgagcagccc	ggngcttctc	cctgcc	2997

<210> 2
 <211> 986
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (283)
 <223> Wherein Xaa is any amino acid.

<220>
 <221> VARIANT
 <222> (792)
 <223> Wherein Xaa is any amino acid.

<400> 2
 Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met

1	5	10	15
Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln	20	25	30
Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu	35	40	45
Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser	50	55	60
Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu	65	70	75
Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp	85	90	95
Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln	100	105	110
Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Gln Tyr	115	120	125
Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser	130	135	140
His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser	145	150	155
Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe	165	170	175
His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile	180	185	190
Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro	195	200	205
Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn	210	215	220
Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu	225	230	235
Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg	245	250	255
Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His	260	265	270
Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Xaa Asp Leu Cys Lys Leu	275	280	285
Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys	290	295	300
Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile			

305		310		315		320
Asp Gly Ile Cys Glu Leu Ser Val Val Ser Thr Ser Ala His Met Pro						
	325			330		335
Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys Ser						
	340			345		350
Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu Glu						
	355			360		365
Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln Asn						
	370			375		380
His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn Met						
	385			390		395
Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn Ile						
	405			410		415
Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu Val						
	420			425		430
Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp Gln						
	435			440		445
Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile Leu						
	450			455		460
Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp Thr						
	465			470		475
Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser Cys						
	485			490		495
Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala His						
	500			505		510
Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn Met						
	515			520		525
Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly Arg						
	530			535		540
Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His Lys						
	545			550		555
Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys Pro						
	565			570		575
Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr Asp						
	580			585		590
Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu Cys						
	595			600		605
Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His Arg						

610					615					620					
Ile	Gly	Arg	Lys	Cys	Glu	Thr	Lys	Phe	Met	Pro	Ala	Ala	Glu	Gly	Thr
625					630					635					640
Ile	Cys	Gly	His	Asp	Met	Trp	Cys	Arg	Gly	Gly	Gln	Cys	Val	Lys	Tyr
				645					650					655	
Gly	Asp	Glu	Gly	Pro	Lys	Pro	Thr	His	Gly	His	Trp	Ser	Asp	Trp	Ser
			660					665					670		
Ser	Trp	Ser	Pro	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	His	Arg
		675					680					685			
Ser	Arg	Leu	Cys	Thr	Asn	Pro	Asn	Pro	Ser	His	Gly	Gly	Lys	Phe	Cys
	690					695					700				
Glu	Gly	Ser	Thr	Arg	Thr	Leu	Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys	Pro
705					710					715					720
Arg	Asp	Ser	Val	Asp	Phe	Arg	Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser
				725					730					735	
Arg	Arg	Phe	Arg	Gly	Arg	His	Tyr	Lys	Trp	Lys	Pro	Gln	Asp	Leu	Cys
			740					745					750		
Lys	Leu	Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser
		755					760					765			
Asn	Lys	Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val
	770					775					780				
Cys	Ile	Asp	Gly	Ile	Cys	Glu	Xaa	Gly	Cys	Asp	Asn	Val	Leu	Gly	Ser
785						790					795				800
Asp	Ala	Val	Glu	Asp	Val	Cys	Gly	Val	Cys	Asn	Gly	Asn	Asn	Ser	Ala
				805					810					815	
Cys	Thr	Ile	His	Arg	Gly	Leu	Tyr	Thr	Lys	His	His	His	Thr	Asn	His
			820					825					830		
Tyr	His	Met	Val	Thr	Ile	Pro	Ser	Gly	Ala	Arg	Ser	Ile	Arg	Ile	Tyr
		835					840					845			
Glu	Met	Asn	Val	Ser	Thr	Ser	Tyr	Ile	Ser	Val	Arg	Asn	Ala	Leu	Arg
	850					855					860				
Arg	Tyr	Tyr	Leu	Asn	Gly	His	Trp	Thr	Val	Asp	Trp	Pro	Gly	Arg	Tyr
865						870					875				880
Lys	Phe	Ser	Gly	Thr	Thr	Phe	Asp	Tyr	Arg	Arg	Ser	Tyr	Asn	Glu	Pro
				885					890					895	
Glu	Asn	Leu	Ile	Ala	Thr	Gly	Pro	Thr	Asn	Glu	Thr	Leu	Ile	Val	Glu
			900					905					910		
Leu	Leu	Phe	Gln	Gly	Arg	Asn	Pro	Gly	Val	Ala	Trp	Glu	Tyr	Ser	Met

915	920	925
Pro Arg Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr		
930	935	940
Trp Ala Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg		
945	950	955 960
Cys Leu Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr		
965	970	975
Ala Tyr Ile Ala Leu Ala Phe Leu Glu Ser		
980	985	

<210> 3
 <211> 2433
 <212> DNA
 <213> Homo sapiens

<400> 3

gtggcccccta	gccccctcggga	gcgctccttg	atgaagcccc	gcgcgcgcgcg	atggcggggc	60
ttggcggcg	tgtggatgct	gctggcgag	gtggccgagc	aggtgagtc	cgggcgctcc	120
caccagcgcg	gaaaccgcgg	gtccggacag	ctggaggcga	gtccccgcg	gctcctctcc	180
cgcgacccc	gccgtctcac	cgcatgtcg	ccgctgtttt	ccgcaggcac	ctgcgtgcgc	240
catgggaccc	gcagcggcag	cgctgggag	cccagcgtc	ccgcgtcctc	ctccaccgc	300
ggagcggccg	ggctggatgg	aaaagggcgg	gacatggatg	aagctggaaa	ccatcgttct	360
cagcaaaata	acacaggaac	agaaaaccaa	acactgcatg	ttctcactcg	tgaatatgac	420
ctggtctctg	cttacgaggt	tgaccacagg	ggcgattacg	tgtcccatga	aatcatgcac	480
catcagcggc	ggagaagagc	agtggccgtg	tccgaggttg	agtctcttca	ccttcggctg	540
aaaggcccca	ggcacgactt	ccacatggat	ctgaggactt	ccagcagcct	agtggctcct	600
ggctttattg	tgcagacgtt	gggaaagaca	ggcactaagt	ctgtgcagac	tttaccgcca	660
gaggactttct	gtttctatca	aggctctttg	cgatcacaca	gaaactcccc	atcgcatgga	720
gggaagtctct	gtgagggctc	cactcgcact	ctgaagctct	gcaacagtca	gaaatgtccc	780
cgggacagtg	ttgacttccg	tgctgctcag	tgtgccgagc	acaacagcag	acgattcaga	840
gggcggcact	acaagtggaa	gccttacact	caagtagaac	aggacttatg	caaactctac	900
tgtatcgcag	aaggatttga	tttcttcttt	tctttgtcaa	ataaagtcaa	agatgggact	960
ccatgctcgg	aggatagccg	taatgtttgt	atagatggga	tatgtgagat	gccccagcct	1020
cccaaggaag	acctcttcat	cttgccagat	gagtataagt	cttgcttacg	gcataagcgc	1080
tctcttctga	ggtcccatag	aaatgaagaa	ctgaacgtgg	agaccttgg	ggtggtcgac	1140
aaaaagatga	tgcaaaacca	tggccatgaa	aatatcacca	cctacgtgct	cacgatactc	1200
aacatggtat	ctgctttatt	caaagatgga	acaataggag	gaaacatcaa	cattgcaatt	1260
gtaggtctga	ttcttctaga	agatgaacag	gacatctgta	aagccctgtg	gtgccatcgt	1320
attggaagga	aatgtgagac	taaaatttatg	ccagcagcag	aaggcacaat	ttgtgggcat	1380
gacatgtggt	gccggggagg	acagtgtgtg	aaatatggtg	atgaaggccc	caagcccacc	1440
catggccact	ggtcggactg	gtcttcttgg	tccccatgct	ccaggacctg	cggaggggga	1500
gtatctcata	ggagtcgcct	ctgcaccaac	cccaggccat	cgcatggagg	gaagttctgt	1560
gagggctcca	ctcgcactct	gaagctctgc	aacagtcaga	aatgtccccg	ggacagtgtt	1620
gacttccgtg	ctgctcagtg	tgccgagcac	aacagcagac	gattcagagg	gcggcactac	1680
aagtggaaagc	ctcaggactt	atgcaaaactc	tactgtatcg	cagaaggatt	tgatttcttc	1740
ttttctttgt	caaataaagt	caaagatggg	actccatgct	cggaggatag	ccgtaatgtt	1800
tgtatagatg	ggatagtga	gggatgtgac	aatgtccttg	gatctgatgc	tgttgaagac	1860
gtctgtgggg	tgtgtaacgg	gaataactca	gectgcacga	ttcacagggg	tctctacacc	1920
aagcaccacc	acaccaacta	ttatcacatg	gtcaccattc	cttctggagc	ccggagtatc	1980
cgcactctatg	aaatgaacgt	ctctacctcc	tacatttctg	tgcgcaatgc	cctcagaagg	2040
tactacctga	atgggcactg	gaccgtggac	tggcccgcc	ggtacaaatt	ttcgggcact	2100
actttcgact	acagacggtc	ctataatgag	cccagagaact	taatcgctac	tggaaccaacc	2160

```

aacgagacac tgattgtgga gctgctgttt caggggaagga acccggtgtg tgcctgggaa 2220
tactccatgc ctcgcttggg gaccgagaag cagccccctg cccagcccag ctacacttgg 2280
gccatcgctg gctctgagtg ctccgtgtcc tgcggagggg gtaggtgcct tccagtgtcg 2340
ctcctggagg cagcatgtca gccttcagcc actgcgtaca ttgcactggc ctttcttgaa 2400
tcctaataag cagccccggg cttctccctg cca 2433

```

<210> 4

<211> 791

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met
  1             5             10             15

Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
      20             25             30

Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
      35             40             45

Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
      50             55             60

Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
      65             70             75             80

Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
      85             90             95

Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
      100            105            110

Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Arg Glu
      115            120            125

Tyr Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val
      130            135            140

Ser His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val
      145            150            155            160

Ser Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp
      165            170            175

Phe His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe
      180            185            190

Ile Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu
      195            200            205

Pro Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg
      210            215            220

Asn Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr
      225            230            235            240

```


Leu Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe
 245 250 255
 Arg Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg
 260 265 270
 His Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Gln Asp Leu Cys Lys
 275 280 285
 Leu Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn
 290 295 300
 Lys Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys
 305 310 315 320
 Ile Asp Gly Ile Cys Glu Met Pro Gln Pro Pro Lys Glu Asp Leu Phe
 325 330 335
 Ile Leu Pro Asp Glu Tyr Lys Ser Cys Leu Arg His Lys Arg Ser Leu
 340 345 350
 Leu Arg Ser His Arg Asn Glu Glu Leu Asn Val Glu Thr Leu Val Val
 355 360 365
 Val Asp Lys Lys Met Met Gln Asn His Gly His Glu Asn Ile Thr Thr
 370 375 380
 Tyr Val Leu Thr Ile Leu Asn Met Val Ser Ala Leu Phe Lys Asp Gly
 385 390 395 400
 Thr Ile Gly Gly Asn Ile Asn Ile Ala Ile Val Gly Leu Ile Leu Leu
 405 410 415
 Glu Asp Glu Gln Asp Ile Cys Lys Ala Leu Trp Cys His Arg Ile Gly
 420 425 430
 Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly Thr Ile Cys
 435 440 445
 Gly His Asp Met Trp Cys Arg Gly Gly Gln Cys Val Lys Tyr Gly Asp
 450 455 460
 Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp Ser Ser Trp
 465 470 475 480
 Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His Arg Ser Arg
 485 490 495
 Leu Cys Thr Asn Pro Arg Pro Ser His Gly Gly Lys Phe Cys Glu Gly
 500 505 510
 Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp
 515 520 525
 Ser Val Asp Phe Arg Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg
 530 535 540

Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Gln Asp Leu Cys Lys Leu
545 550 555 560

Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys
565 570 575

Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile
580 585 590

Asp Gly Ile Cys Glu Gly Cys Asp Asn Val Leu Gly Ser Asp Ala Val
595 600 605

Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile
610 615 620

His Arg Gly Leu Tyr Thr Lys His His His Thr Asn Tyr Tyr His Met
625 630 635 640

Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met Asn
645 650 655

Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr Tyr
660 665 670

Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe Ser
675 680 685

Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn Leu
690 695 700

Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu Phe
705 710 715 720

Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg Leu
725 730 735

Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala Ile
740 745 750

Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu Pro
755 760 765

Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr Ala Tyr Ile
770 775 780

Ala Leu Ala Phe Leu Glu Ser
785 790

<210> 5

<211> 2902

<212> DNA

<213> Homo sapiens

<400> 5

ttggcgggcgc tgtggatgct gctggcgagc gtggccgagc aggtgagtcc cgggcgctcc 60

caccagcgcg	gaaaccgcg	gtccggacag	ctggaggcga	gtcccccg	gctcctctcc	120
cgcggaaccc	gccgtctcac	cgcgatgtcg	ccgctgtttt	ccgcaggcac	ctgcgtgcgc	180
catgggaccc	gcagcggcag	cgccctggag	cccagacgtc	ccgcgtcctc	ctccagacct	240
ggtctctgcc	tacgagggtg	accacagggg	cgattacgtg	tcccatgaaa	tcatgcacca	300
tcagcggcgg	agaagagcag	tggccgtgtc	cgagggtgag	ccagcctttc	tccaggtatg	360
cagagccaga	gagctcagac	tgtgtgtgga	ggcctttccc	attgctaatt	ctcagccggg	420
gtttttgaac	ctttccaatg	ttcgctctca	ctggagggaa	cagcatgctt	ccaagagaat	480
aataacaaat	gcaatgcttg	gagaatcggc	cctggcttca	accagaaagt	ctaattgtgt	540
tttctttctt	tccttttatt	ttttccagtc	aggcatgata	cgaacagaag	aggcagatta	600
cttcctaagg	ccacttcctt	cacacctctc	atggaaactc	ggcagagctg	cccaaggcag	660
ctcgccatcc	cacgtactgt	acaagagaga	ggtcctggtg	acctcaagga	catgggagct	720
ggcacatcaa	cccctgcaca	gcagcgacct	tcgcctggga	ctgccacaaa	agcagcattt	780
ctgtggaaga	cgcaagaaat	acatgcccc	gcctcccaag	gaagacctct	tcatcttgcc	840
agatgagtat	aagtcttgct	tacggcataa	gcgctctctt	ctgagggtccc	atagaaatga	900
agaactgaac	gtggagacct	tgggtggtgt	cgacaaaaag	atgatgcaaa	accatggcca	960
tgaaaatatc	accacctacg	tgtcacgat	actcaacatg	gtatctgctt	tattcaaaga	1020
tggaacaata	ggaggaaaca	tcaacattgc	aattgtaggt	ctgattcttc	tagaagatga	1080
acagccagga	ctggtgataa	gtcaccacgc	agaccacacc	ttaagtagtt	tctgccagtg	1140
gcagtctgga	ttgatgggga	aagatgggac	tcgtcatgac	cacgccatct	tactgactgg	1200
tctggatata	tgttcctgga	agaatgagcc	ctgtgacact	ttgggatttg	cacccataag	1260
tggaatgtgt	agtaaatatc	gcagctgcac	gattaatgaa	gatacaggtc	ttggactggc	1320
cttcaccatt	gcccctgagt	ctggacacaa	ctttggcatg	attcatgatg	gagaagggaa	1380
catgtgcaaa	aagtcggagg	gcaacatcat	gtcccctaca	ttggcaggac	gcaatggagt	1440
cttctcctgg	tcacctgca	gccgccagta	tctacacaaa	tttctaagca	ccgctcaagc	1500
tatctgcctt	gctgatcagc	caaagcctgt	gaaggaaatac	aagtatcctg	agaaattgcc	1560
aggagaatta	tatggtgcaa	acacacagtg	caagtggcag	ttcggagaga	aagccaagct	1620
ctgcatgctg	gactttaaaa	aggacatctg	taaagccctg	tggtgccatc	gtattggaag	1680
gaaatgtgag	actaaattta	tgccagcagc	agaaggcaca	atttgtgggc	atgaacatgg	1740
tgccggaggga	cagtgtgtga	aatatggtga	tgaaggcccc	aagccccacc	atggccactg	1800
gtcggactgg	tcttcttggt	ccccatgctc	caggacctgc	ggagggggag	tatctcatag	1860
gagtcgctct	caaaatacac	attccaggcc	atcgcatgga	gggaagttct	gtgagggtct	1920
cactcgcact	ctgaagctct	gcaacagtca	gaaatgtccc	cgggacagtg	ttgacttccg	1980
tgctgctcag	tgtgccgagc	acaacagcag	acgattcaga	gggcggcact	acaagtggaa	2040
gcctgatcag	gacttatgca	aactctactg	tatcgcagaa	ggatttgatt	tcttcttttc	2100
tttgtcaaat	aaagtcaaag	atgggactcc	atgctcggag	gatagccgta	atgtttgtat	2160
agatgggata	tgtgagagag	ttggatgtga	caatgtcctt	ggatctgatg	ctgttgaaga	2220
cgtctgtggg	gtgtgtaacg	ggaataactc	agcctgcacg	attcacaggg	gtctctacct	2280
agagtattat	cacatggtca	ccattccttc	tggagcccg	agtatccgca	tctatgaaat	2340
gaacgtctct	acctcctaca	tttctgtgcg	caatgcctc	agaaggtact	acctgaatgg	2400
gcactggacc	gtggactggc	ccggccggta	caaattttcg	ggcactactt	tcgactacag	2460
acggtcctat	aatgagccc	agaacttaat	cgctactgga	ccaaccaacg	agacactgat	2520
tgtggagctg	ctgtttcagg	gaaggaaccc	gggtgttgcc	tgggaatact	ccatgcctcg	2580
cttggggacc	gagaagcagc	cccctgcccc	gccagctac	acttgggcca	tcgtgcgctc	2640
tgagtgcctc	gtgtcctgcg	gagggggtag	gtgccttcca	gtgctgctcc	tggaggcagc	2700
atgtcagcct	ttagccactg	cgtacattgc	actggccttt	cttgaatcct	aatgagcagc	2760
ccggggcttc	tccttgccag	tagcagtgac	attcccaagg	tggggagtgg	tggtcctgag	2820
tgtcacttgt	cggcccagc	tgccttctcc	agtctatctg	cttcagtgtg	tgactctgag	2880
gaagtcagta	gatgcattgc	tt				2902

<210> 6

<211> 856

<212> PRT

<213> Homo sapiens

<400> 6

Met Gly Pro Ala Ala Ala Ala Pro Gly Ser Pro Ser Val Pro Arg Pro

1	5	10	15
Pro Pro Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr	20	25	30
Val Ser His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala	35	40	45
Val Ser Glu Val Glu Pro Ala Phe Leu Gln Val Cys Arg Ala Arg Glu	50	55	60
Leu Arg Leu Cys Val Glu Ala Phe Pro Ile Ala Asn Ser Gln Pro Gly	65	70	75
Phe Leu Asn Leu Ser Asn Val Arg Ser His Trp Arg Glu Gln His Ala	85	90	95
Ser Lys Arg Ile Ile Thr Asn Ala Met Leu Gly Glu Ser Ala Leu Ala	100	105	110
Ser Thr Arg Lys Ser Asn Cys Val Phe Phe Leu Ser Phe Tyr Phe Phe	115	120	125
Gln Ser Gly Met Ile Arg Thr Glu Glu Ala Asp Tyr Phe Leu Arg Pro	130	135	140
Leu Pro Ser His Leu Ser Trp Lys Leu Gly Arg Ala Ala Gln Gly Ser	145	150	155
Ser Pro Ser His Val Leu Tyr Lys Arg Glu Val Leu Val Thr Ser Arg	165	170	175
Thr Trp Glu Leu Ala His Gln Pro Leu His Ser Ser Asp Leu Arg Leu	180	185	190
Gly Leu Pro Gln Lys Gln His Phe Cys Gly Arg Arg Lys Lys Tyr Met	195	200	205
Pro Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys	210	215	220
Ser Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu	225	230	235
Glu Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln	245	250	255
Asn His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn	260	265	270
Met Val Ser Ala Leu Phe Lys Asp Gly Thr Ile Gly Gly Asn Ile Asn	275	280	285
Ile Ala Ile Val Gly Leu Ile Leu Leu Glu Asp Glu Gln Pro Gly Leu	290	295	300
Val Ile Ser His His Ala Asp His Thr Leu Ser Ser Phe Cys Gln Trp			

305		310		315		320
Gln Ser Gly Leu Met Gly Lys Asp Gly Thr Arg His Asp His Ala Ile						
		325		330		335
Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys Asn Glu Pro Cys Asp						
		340		345		350
Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys Ser Lys Tyr Arg Ser						
		355		360		365
Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu Ala Phe Thr Ile Ala						
		370		375		380
His Glu Ser Gly His Asn Phe Gly Met Ile His Asp Gly Glu Gly Asn						
		385		390		400
Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser Pro Thr Leu Ala Gly						
		405		410		415
Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser Arg Gln Tyr Leu His						
		420		425		430
Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu Ala Asp Gln Pro Lys						
		435		440		445
Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu Pro Gly Glu Leu Tyr						
		450		455		460
Gly Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly Glu Lys Ala Lys Leu						
		465		470		475
Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys Ala Leu Trp Cys His						
		485		490		495
Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met Pro Ala Ala Glu Gly						
		500		505		510
Thr Ile Cys Gly His Glu His Gly Ala Gly Gly Gln Cys Val Lys Tyr						
		515		520		525
Gly Asp Glu Gly Pro Lys Pro Thr His Gly His Trp Ser Asp Trp Ser						
		530		535		540
Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly Gly Gly Val Ser His Arg						
		545		550		555
Ser Arg Ser Gln Asn Thr His Ser Arg Pro Ser His Gly Gly Lys Phe						
		565		570		575
Cys Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys Asn Ser Gln Lys Cys						
		580		585		590
Pro Arg Asp Ser Val Asp Phe Arg Ala Ala Gln Cys Ala Glu His Asn						
		595		600		605
Ser Arg Arg Phe Arg Gly Arg His Tyr Lys Trp Lys Pro Asp Gln Asp						

610					615					620					
Leu	Cys	Lys	Leu	Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser
625					630					635					640
Leu	Ser	Asn	Lys	Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg
			645						650					655	
Asn	Val	Cys	Ile	Asp	Gly	Ile	Cys	Glu	Arg	Val	Gly	Cys	Asp	Asn	Val
			660					665					670		
Leu	Gly	Ser	Asp	Ala	Val	Glu	Asp	Val	Cys	Gly	Val	Cys	Asn	Gly	Asn
		675					680					685			
Asn	Ser	Ala	Cys	Thr	Ile	His	Arg	Gly	Leu	Tyr	Leu	Glu	Tyr	Tyr	His
	690					695					700				
Met	Val	Thr	Ile	Pro	Ser	Gly	Ala	Arg	Ser	Ile	Arg	Ile	Tyr	Glu	Met
705						710					715				720
Asn	Val	Ser	Thr	Ser	Tyr	Ile	Ser	Val	Arg	Asn	Ala	Leu	Arg	Arg	Tyr
			725						730					735	
Tyr	Leu	Asn	Gly	His	Trp	Thr	Val	Asp	Trp	Pro	Gly	Arg	Tyr	Lys	Phe
			740					745					750		
Ser	Gly	Thr	Thr	Phe	Asp	Tyr	Arg	Arg	Ser	Tyr	Asn	Glu	Pro	Glu	Asn
		755					760					765			
Leu	Ile	Ala	Thr	Gly	Pro	Thr	Asn	Glu	Thr	Leu	Ile	Val	Glu	Leu	Leu
	770					775					780				
Phe	Gln	Gly	Arg	Asn	Pro	Gly	Val	Ala	Trp	Glu	Tyr	Ser	Met	Pro	Arg
785				790						795					800
Leu	Gly	Thr	Glu	Lys	Gln	Pro	Pro	Ala	Gln	Pro	Ser	Tyr	Thr	Trp	Ala
				805					810					815	
Ile	Val	Arg	Ser	Glu	Cys	Ser	Val	Ser	Cys	Gly	Gly	Gly	Arg	Cys	Leu
			820					825					830		
Pro	Val	Leu	Leu	Leu	Glu	Ala	Ala	Cys	Gln	Pro	Leu	Ala	Thr	Ala	Tyr
		835					840					845			
Ile	Ala	Leu	Ala	Phe	Leu	Glu	Ser								
	850					855									

<210> 7

<211> 2895

<212> DNA

<213> Homo sapiens

<400> 7

cgctcctgga tgaagccccg cgcgcgcgga tggcggggct tggcggcgct gtggatgctg 60
 ttggcgcagg tggccgagca ggtgagtccc gggcgctccc accagcgcgg aaaccgcggg 120
 tccggacagc tggaggcgag tccccgcgg ctcctctccc gcggaccccc cgtctcacc 180

gcgatgtcgc	cgctgttttc	cgcaggcacc	tgcgtgcgcc	atgggacccg	cagcggcagc	240
gcctgggagc	ccgagcgtcc	cgcgtccctc	tccaccgcgc	gagcggccgg	gctggatgga	300
aaagggcggg	acatggatga	agctggaaac	catcgtttct	agcaaactaa	cacaggaaca	360
gaaaacccaa	cactgcatgt	tctcactcaa	tatgacctgg	tctctgccta	cgaggttgac	420
cacaggggcg	attacgtgtc	ccatgaaatc	atgcaccatc	agcggcggag	aagagcagtg	480
gccgtgtccg	agggttagtc	tcttcacctt	cggctgaaag	gccccaggca	cgacttccac	540
atggatctga	ggacttccag	cagcctagtg	gctcctggct	ttattgtgca	gacgttggga	600
aagacaggca	ctaagtctgt	gcagacttta	ccgccagagg	acttctgttt	ctatcaaggc	660
tctttgcgat	cacacagaaa	ctcgccatcg	catggaggga	agttctgtga	gggctccact	720
cgcactctga	agctctgcaa	cagtcagaaa	tgtccccggg	acagtgttga	cttccgtgct	780
gctcagtgtg	ccgagcacia	cagcagacga	ttcagagggc	ggcactacaa	gtggaagcct	840
tacactcaag	tagaagccga	cttatgcaaa	ctctactgta	tgcgagaagg	atttgatttc	900
ttcttttctt	tgtcaaataa	agtcaaagat	gggactccat	gctcggagga	tagccgtaat	960
gtttgtatag	atgggatatg	tgagctcagt	gtggtgtcca	catctgcgca	catgccccag	1020
cctcccaagg	aagacctctt	catcttgcca	gatgagtata	agtcttgctt	acggcataag	1080
cgctctcttc	tgaggtccca	tagaaatgaa	gaactgaacg	tggagacctt	gggtggtggtc	1140
gacaaaaaga	tgatgcaaaa	ccatggccat	gaaaatatca	ccacctacgt	gctcacgata	1200
ctcaacatgg	tatctgcttt	attcaaagat	ggattgatgg	ggaaagatgg	gactcgtcat	1260
gaccacgcca	tcttactgac	tggtctggat	atatgttccct	ggaagaatga	gccctgtgac	1320
actttgggat	ttgcacccat	aagtggaatg	tgtagtaaag	atcgcagctg	cacgattaat	1380
gaagatacag	gtcttggact	ggccttcacc	attgcccatt	agtctggaca	caactttggc	1440
atgattcatg	atggagaagg	gaacatgtgt	aaaaagtccg	agggcaacat	catgtcccct	1500
acattggcag	gacgcaatgg	agtcttctcc	tggtcaccct	gcagccgcca	gtatctacac	1560
aaattttctaa	gcaccgctca	agctatctgc	cttgtctgatc	agccaaagcc	tgtgaaggaa	1620
tacaagtatc	ctgagaaatt	gccaggagaa	ttatatgatg	caaacacaca	gtgcaagtgg	1680
cagttcggag	agaaagccaa	gctctgcatg	ctggacttta	aaaaggacat	ctgtaaagcc	1740
ctgtggtgcc	atcgtattgg	aaggaaatgt	gagactaaat	ttatgccagc	agcagaaggc	1800
acaatttgtg	ggcatgacat	gtggtgccgg	ggaggacagt	gtgtgaaata	tggtgatgaa	1860
ggccccaagc	ccaccttggt	ccactggctg	gactggctct	cttgggtccc	atgctccagg	1920
acctgcgagg	ggggagtatc	tcataggagt	cgcctctgca	ccaaccccaa	gccatcgcat	1980
ggagggaagt	tctgtgaggg	ctccactcgc	actctgaagc	tctgcaacag	tcagaaatgt	2040
ccccgggaca	gtggtgactt	ccgtgctgct	cagtgtgccg	agcacaacag	cagacgattc	2100
agagggcggc	actacaagtg	gaagccttac	actcaagtag	aagatcagga	cttatgcaaa	2160
ctctactgta	tgcgagaagg	atttgatttc	ttcttttctt	tgtcaaataa	agtcaaagat	2220
gggactccat	gctcggagga	tagccgtaat	gtttgtatag	atgggatatg	tgagagagtt	2280
ggatgtgaca	atgtccttgg	atctgatgct	gttgaagacg	tctgtggggg	gtgtaacggg	2340
aataactcag	cctgcacgat	tcacaggggt	ctctacacca	agcaccacca	caccaaccag	2400
tattatcaca	tggtcaccat	tccttctgga	gcccggagta	tccgcatcta	tgaaatgaac	2460
gtctctacct	cctacatttc	tgtgcgcaat	gccctcagaa	ggtactacct	gaatgggcac	2520
tggaaccgtg	actggcccgg	ccggtacaaa	ttttcgggca	ctactttcga	ctacagacgg	2580
tcctataatg	agcccagagaa	cttaatcgct	actggaccaaa	ccaacgagac	actgattgtg	2640
gagctgctgt	ttcaggggaag	gaacccgggt	gttgccctggg	aatactccat	gcctcgcttg	2700
gggaccgaga	agcagccccc	tgcccagccc	agctacactt	gggccatcgt	gcgctctgag	2760
tgctccgtgt	cctgcggagg	gggtaggtgc	cttcacgtgc	tgctcctgga	ggcagcatgt	2820
cagccttcag	ccactgcgta	cattgcactg	gcctttcttg	aatcctaagt	agcagcccgg	2880
ggctttctccc	tgcca					2895

<210> 8

<211> 952

<212> PRT

<213> Homo sapiens

<400> 8

Met Lys Pro Arg Ala Arg Gly Trp Arg Gly Leu Ala Ala Leu Trp Met

1

5

10

15

Leu Leu Ala Gln Val Ala Glu Gln Val Ser Pro Gly Arg Ser His Gln
 20 25 30
 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu
 35 40 45
 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser
 50 55 60
 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu
 65 70 75 80
 Pro Glu Arg Pro Ala Ser Ser Ser Thr Arg Gly Ala Ala Gly Leu Asp
 85 90 95
 Gly Lys Gly Arg Asp Met Asp Glu Ala Gly Asn His Arg Ser Gln Gln
 100 105 110
 Thr Asn Thr Gly Thr Glu Asn Gln Thr Leu His Val Leu Thr Gln Tyr
 115 120 125
 Asp Leu Val Ser Ala Tyr Glu Val Asp His Arg Gly Asp Tyr Val Ser
 130 135 140
 His Glu Ile Met His His Gln Arg Arg Arg Arg Ala Val Ala Val Ser
 145 150 155 160
 Glu Val Glu Ser Leu His Leu Arg Leu Lys Gly Pro Arg His Asp Phe
 165 170 175
 His Met Asp Leu Arg Thr Ser Ser Ser Leu Val Ala Pro Gly Phe Ile
 180 185 190
 Val Gln Thr Leu Gly Lys Thr Gly Thr Lys Ser Val Gln Thr Leu Pro
 195 200 205
 Pro Glu Asp Phe Cys Phe Tyr Gln Gly Ser Leu Arg Ser His Arg Asn
 210 215 220
 Ser Pro Ser His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu
 225 230 235 240
 Lys Leu Cys Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg
 245 250 255
 Ala Ala Gln Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His
 260 265 270
 Tyr Lys Trp Lys Pro Tyr Thr Gln Val Glu Ala Asp Leu Cys Lys Leu
 275 280 285
 Tyr Cys Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys
 290 295 300
 Val Lys Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile
 305 310 315 320

Asp Gly Ile Cys Glu Leu Ser Val Val Ser Thr Ser Ala His Met Pro
 325 330 335
 Gln Pro Pro Lys Glu Asp Leu Phe Ile Leu Pro Asp Glu Tyr Lys Ser
 340 345 350
 Cys Leu Arg His Lys Arg Ser Leu Leu Arg Ser His Arg Asn Glu Glu
 355 360 365
 Leu Asn Val Glu Thr Leu Val Val Val Asp Lys Lys Met Met Gln Asn
 370 375 380
 His Gly His Glu Asn Ile Thr Thr Tyr Val Leu Thr Ile Leu Asn Met
 385 390 395 400
 Val Ser Ala Leu Phe Lys Asp Gly Leu Met Gly Lys Asp Gly Thr Arg
 405 410 415
 His Asp His Ala Ile Leu Leu Thr Gly Leu Asp Ile Cys Ser Trp Lys
 420 425 430
 Asn Glu Pro Cys Asp Thr Leu Gly Phe Ala Pro Ile Ser Gly Met Cys
 435 440 445
 Ser Lys Tyr Arg Ser Cys Thr Ile Asn Glu Asp Thr Gly Leu Gly Leu
 450 455 460
 Ala Phe Thr Ile Ala His Glu Ser Gly His Asn Phe Gly Met Ile His
 465 470 475 480
 Asp Gly Glu Gly Asn Met Cys Lys Lys Ser Glu Gly Asn Ile Met Ser
 485 490 495
 Pro Thr Leu Ala Gly Arg Asn Gly Val Phe Ser Trp Ser Pro Cys Ser
 500 505 510
 Arg Gln Tyr Leu His Lys Phe Leu Ser Thr Ala Gln Ala Ile Cys Leu
 515 520 525
 Ala Asp Gln Pro Lys Pro Val Lys Glu Tyr Lys Tyr Pro Glu Lys Leu
 530 535 540
 Pro Gly Glu Leu Tyr Asp Ala Asn Thr Gln Cys Lys Trp Gln Phe Gly
 545 550 555 560
 Glu Lys Ala Lys Leu Cys Met Leu Asp Phe Lys Lys Asp Ile Cys Lys
 565 570 575
 Ala Leu Trp Cys His Arg Ile Gly Arg Lys Cys Glu Thr Lys Phe Met
 580 585 590
 Pro Ala Ala Glu Gly Thr Ile Cys Gly His Asp Met Trp Cys Arg Gly
 595 600 605
 Gly Gln Cys Val Lys Tyr Gly Asp Glu Gly Pro Lys Pro Thr His Gly
 610 615 620

His Trp Ser Asp Trp Ser Ser Trp Ser Pro Cys Ser Arg Thr Cys Gly
 625 630 635 640
 Gly Gly Val Ser His Arg Ser Arg Leu Cys Thr Asn Pro Lys Pro Ser
 645 650 655
 His Gly Gly Lys Phe Cys Glu Gly Ser Thr Arg Thr Leu Lys Leu Cys
 660 665 670
 Asn Ser Gln Lys Cys Pro Arg Asp Ser Val Asp Phe Arg Ala Ala Gln
 675 680 685
 Cys Ala Glu His Asn Ser Arg Arg Phe Arg Gly Arg His Tyr Lys Trp
 690 695 700
 Lys Pro Tyr Thr Gln Val Glu Asp Gln Asp Leu Cys Lys Leu Tyr Cys
 705 710 715 720
 Ile Ala Glu Gly Phe Asp Phe Phe Phe Ser Leu Ser Asn Lys Val Lys
 725 730 735
 Asp Gly Thr Pro Cys Ser Glu Asp Ser Arg Asn Val Cys Ile Asp Gly
 740 745 750
 Ile Cys Glu Arg Val Gly Cys Asp Asn Val Leu Gly Ser Asp Ala Val
 755 760 765
 Glu Asp Val Cys Gly Val Cys Asn Gly Asn Asn Ser Ala Cys Thr Ile
 770 775 780
 His Arg Gly Leu Tyr Thr Lys His His His Thr Asn Gln Tyr Tyr His
 785 790 795 800
 Met Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met
 805 810 815
 Asn Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr
 820 825 830
 Tyr Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe
 835 840 845
 Ser Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn
 850 855 860
 Leu Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu
 865 870 875 880
 Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg
 885 890 895
 Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala
 900 905 910
 Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu
 915 920 925

Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr Ala Tyr
 930 935 940

Ile Ala Leu Ala Phe Leu Glu Ser
 945 950

<210> 9
 <211> 4488
 <212> DNA
 <213> Homo sapiens

<400> 9
 atgtgggctc agctccttct aggaatgttg gccctatcac cagccattgc agaagaactt 60
 ccaaactacc tggtagacatt accagcccgg ctaaatttcc cctccgttca gaaggtttgt 120
 ttggacctga gccctgggta cagtgatgtt aaattcacgg ttactctgga gaccaaggac 180
 aagaccaga agttgctaga atactctgga ctgaagaaga ggcacttaca ttgtatctcc 240
 tttcttgtac cacctcctgc tggtagcaca gaagaagtgg ccacaatccg ggtgtcggga 300
 gttggaaata acatcagctt tgaggagaag aaaaagggtc taattcagag gcaggggaac 360
 ggcacctttg tacagactga caaacctctc tacaccccag ggcagcaagt gtatttccgc 420
 attgtcacca tggatagcaa cttcgttcca gtgaatgaca agtactccat ggtggaacta 480
 caggatccaa atagcaacag gattgcacag tggctggaag tggtagctga gcaaggcatt 540
 gtagacctgt ccttccaact ggcaccagag gcaatgctgg gcacctacac tgtggcagtg 600
 gctgagggca agacctttgg tactttcagt gtggaggaat atgtgctttc tccatttctc 660
 cttttactct cttcagtgtc gccgaagttt aagggtggaag tggtagaacc caaggagtta 720
 tcaacggtgc aggaatcttt cttagtataa atttgttgta ggtacaccta tggaaagccc 780
 atgctagggg cagtgcaggt atctgtgtgt cagaaggcaa atacttactg gtatcgagag 840
 gtggaacggg aacagcttcc tgacaaatgc aggaacctct ctggacagac tgacaaaaca 900
 ggatgtttct cagcacctgt ggacatggcc acctttgacc tcattggata tgcgtacagc 960
 catcaaatca atattgtggc tactgttgtg gaggaaggga caggtgtgga ggccaatgcc 1020
 actcagaata tctacatttc tccacaaatg ggatcaatga cctttgaaga caccagcaat 1080
 ttttaccatc caaatttccc cttcagtggt aagatgctgc tcaagtttcc gcaaggcggg 1140
 gtgctccctt gcaagaacca tctagtgttt ctggtgattt atggcacaaa tggaaacctt 1200
 aaccagaccc tggttactga taacaatggc ctagctccct ttaccttga gacatccggg 1260
 tggaaatggga cagacgtttc tctggaggga aagtttcaaa tggaaagactt agtatataat 1320
 ccggaacaag tgccacgtta ctacaaaat gcctacctgc acctgcgacc cttctacagc 1380
 acaaccgcga gcttccttgg catccaccgg ctaaaccggc ccttgaaatg tggccagccc 1440
 caggaagtgc tggtaggatta ttacatcgac ccggccgatg caagccctga ccaagagatc 1500
 agcttctcct actattttaat agggaaagga agtttgggtga tggaggggca gaaacacctg 1560
 aactctaaga agaaaggact gaaagcctcc ttctctctct cactgacctt cacttcgaga 1620
 ctggccccctg atccttccct ggtgatctat gccatttttc ccagtggagg tgtttagct 1680
 gacaaaattc agttctcagt cgagatgtgc tttgacaatc agcagcttcc aggagcagaa 1740
 gtggagctgc agctgcaggc agctcccggg tccctgtgtg cgctccgggc ggtggatgag 1800
 agtgtcttac tgcttaggcc agacagagag ctgagcaacc gctctgtcta tgggatgttt 1860
 ccattctggg atggtcacta cccctatcaa gtggctgagt atgatcagt tccagtgtct 1920
 ggcccatggg actttcctca gccctcatt gacccaatgc cccaagggca ttcgagccag 1980
 cgttccatta tctggaggcc ctcgttctct gaaggcacgg accttttcag ctttttccgg 2040
 gacgtgggccc tgaaaatact gtccaatgcc aaaatcaaga agccagtaga ttgcagtcac 2100
 agatctccag aatacagcac tgctatgggt ggcggtgggt atccagaggc ttttgagtca 2160
 tcaactcctt tacatcaagc agaggattct caggtccgcc agtacttccc agagacctgg 2220
 ctctgggacg tgtttcctat tggtaactcg gggaaggagg cgggccacgt cacagttcct 2280
 gacgccatca ccgagtggaa ggcatgagt ttctgcaact cccagtcaag aggttccggg 2340
 ctttcaccca ctgttggaact aactgctttc aagccgttct ttgttgacct gactctccct 2400
 tactcagtag tccgtgggga atcctttcgt cttactgcca ccatcttcaa ttacctaaag 2460
 gattgcatca gggttcagac tgacctggct aaatcgcatg agtaccagct agaatcatgg 2520
 gcagattctc agacctccag ttgtctctgt gctgatgacg caaaaacca ccaactggaac 2580
 atcacagctg tcaaatggg tcaatattaac ttactatta gtacaaagat tctggacagc 2640

```

aatgaaccat gtggggggcca gaagggggttt gttccccaaa agggccgaag tgacacgctc 2700
atcaagccag ttctcgtcaa acctgagggg gtcctgggtg agaagacaca cagctcattg 2760
ctgtgcccaa aaggaggaaa ggtggcatct gaatctgtct ccctggagct cccagtggac 2820
attgttcctg actcgaccaa ggcttatgtt acggttcttg gagacattat gggcacagcc 2880
ctgcagaacc tggatggtct ggtgcagatg cccagtggct gtggcgagca gaacatggtc 2940
ttgtttgctc ccatcatcta tgtcttgcat tacctggaga aggcagggtc gctgacggag 3000
gagatcaggt ctcgggcagt gggtttcctg gaaatagggt accagaagga gctgatgtac 3060
aaacacagca atggctcata cagtgccttt ggggagcgag atggaaatgg aaacacatgg 3120
ctgacagcgt ttgtcacaaa atgctttggc caagctcaga aattcatctt cattgatccc 3180
aagaacatcc aggatgctct caagtggatg gcaggaaacc agtccccag tggctgctat 3240
gccaacgtgg gaaatctcct tcacacagct atgaagggtg gtgttgatga tgaggtctcc 3300
ttgactgcgt atgtcacagc tgcattgctg gagatgggaa aggatgtaga tgaccaatg 3360
gtgagtcagg gtctacggtg tctcaagaat tcggccacct ccacgaccaa cctctacaca 3420
caggccctgt tggcttacat tttctccctg gctggggaaa tggacatcag aaacattctc 3480
cttaaacagt tagatcaaca ggctatcatc tcaggagaat ccatttactg gagccagaaa 3540
cctactccat catcgaacgc cagcccttgg tctgagcctg cggctgtaga tgtggaactc 3600
acagcatatg cattgttggc ccagcttacc aagcccagcc tgactcaaaa ggagatagcg 3660
aaggccacta gcatagtggc ttggttggcc aagcaacaca atgcatatgg gggcttctct 3720
tctactcagg atactgtagt tgctctccaa gctcttgcca aatatgccac taccgcctac 3780
atgccatctg aggagatcaa cctggttgta aaatccactg agaatttcca gcgcacattc 3840
aacatacagt cagttaacag attggtatct cagcaggata ccctgccccaa tgtccctgga 3900
atgtacacgt tggaggcctc aggccagggc tgtgtctatg tgcagacggt gttgagatac 3960
aatattctcc ctcccacaaa tatgaagacc tttagtctta gtgtggaaat aggaaaagct 4020
agatgtgagc aaccgacttc acctcgatcc ttgactctca ctattcacac cagttatgtg 4080
gggagccgta gctcttccaa tatggctatt gtggaagtga agatgctatc tgggttcagt 4140
cccatggagg gcaccaatca gttacttctc cagcaacccc tggatgaaga ggttgaattt 4200
ggaactgaca cacttaacat ttacttggat gagctcatta agaacactca gacttacacc 4260
ttcaccatca gccaaagtgt gctggtcacc aacttgaaac cagcaacat caaggtctat 4320
gactactacc taccaggttc ttttaaatta tctcagtaca caattgtgtg gtccatgaac 4380
aatgacagca tagtggactc tgtggcacgg caccagaac cacccttctt caagacagaa 4440
gcatttatcc cttcacttcc tgggagtggt aacaactgat agctacca 4488

```

<210> 10
 <211> 1492
 <212> PRT
 <213> Homo sapiens

```

<400> 10
Met Trp Ala Gln Leu Leu Leu Gly Met Leu Ala Leu Ser Pro Ala Ile
  1              5              10              15

Ala Glu Glu Leu Pro Asn Tyr Leu Val Thr Leu Pro Ala Arg Leu Asn
      20              25              30

Phe Pro Ser Val Gln Lys Val Cys Leu Asp Leu Ser Pro Gly Tyr Ser
      35              40              45

Asp Val Lys Phe Thr Val Thr Leu Glu Thr Lys Asp Lys Thr Gln Lys
      50              55              60

Leu Leu Glu Tyr Ser Gly Leu Lys Lys Arg His Leu His Cys Ile Ser
      65              70              75              80

Phe Leu Val Pro Pro Pro Ala Gly Gly Thr Glu Glu Val Ala Thr Ile
      85              90              95

```

Arg	Val	Ser	Gly	Val	Gly	Asn	Asn	Ile	Ser	Phe	Glu	Glu	Lys	Lys	Lys	100	105	110
Val	Leu	Ile	Gln	Arg	Gln	Gly	Asn	Gly	Thr	Phe	Val	Gln	Thr	Asp	Lys	115	120	125
Pro	Leu	Tyr	Thr	Pro	Gly	Gln	Gln	Val	Tyr	Phe	Arg	Ile	Val	Thr	Met	130	135	140
Asp	Ser	Asn	Phe	Val	Pro	Val	Asn	Asp	Lys	Tyr	Ser	Met	Val	Glu	Leu	145	150	155
Gln	Asp	Pro	Asn	Ser	Asn	Arg	Ile	Ala	Gln	Trp	Leu	Glu	Val	Val	Pro	165	170	175
Glu	Gln	Gly	Ile	Val	Asp	Leu	Ser	Phe	Gln	Leu	Ala	Pro	Glu	Ala	Met	180	185	190
Leu	Gly	Thr	Tyr	Thr	Val	Ala	Val	Ala	Glu	Gly	Lys	Thr	Phe	Gly	Thr	195	200	205
Phe	Ser	Val	Glu	Glu	Tyr	Val	Leu	Ser	Pro	Phe	Leu	Leu	Leu	Leu	Ser	210	215	220
Ser	Val	Leu	Pro	Lys	Phe	Lys	Val	Glu	Val	Val	Glu	Pro	Lys	Glu	Leu	225	230	235
Ser	Thr	Val	Gln	Glu	Ser	Phe	Leu	Val	Lys	Ile	Cys	Cys	Arg	Tyr	Thr	245	250	255
Tyr	Gly	Lys	Pro	Met	Leu	Gly	Ala	Val	Gln	Val	Ser	Val	Cys	Gln	Lys	260	265	270
Ala	Asn	Thr	Tyr	Trp	Tyr	Arg	Glu	Val	Glu	Arg	Glu	Gln	Leu	Pro	Asp	275	280	285
Lys	Cys	Arg	Asn	Leu	Ser	Gly	Gln	Thr	Asp	Lys	Thr	Gly	Cys	Phe	Ser	290	295	300
Ala	Pro	Val	Asp	Met	Ala	Thr	Phe	Asp	Leu	Ile	Gly	Tyr	Ala	Tyr	Ser	305	310	315
His	Gln	Ile	Asn	Ile	Val	Ala	Thr	Val	Val	Glu	Glu	Gly	Thr	Gly	Val	325	330	335
Glu	Ala	Asn	Ala	Thr	Gln	Asn	Ile	Tyr	Ile	Ser	Pro	Gln	Met	Gly	Ser	340	345	350
Met	Thr	Phe	Glu	Asp	Thr	Ser	Asn	Phe	Tyr	His	Pro	Asn	Phe	Pro	Phe	355	360	365
Ser	Gly	Lys	Met	Leu	Leu	Lys	Phe	Pro	Gln	Gly	Gly	Val	Leu	Pro	Cys	370	375	380
Lys	Asn	His	Leu	Val	Phe	Leu	Val	Ile	Tyr	Gly	Thr	Asn	Gly	Thr	Phe	385	390	395

Asn Gln Thr Leu Val Thr Asp Asn Asn Gly Leu Ala Pro Phe Thr Leu
 405 410 415
 Glu Thr Ser Gly Trp Asn Gly Thr Asp Val Ser Leu Glu Gly Lys Phe
 420 425 430
 Gln Met Glu Asp Leu Val Tyr Asn Pro Glu Gln Val Pro Arg Tyr Tyr
 435 440 445
 Gln Asn Ala Tyr Leu His Leu Arg Pro Phe Tyr Ser Thr Thr Arg Ser
 450 455 460
 Phe Leu Gly Ile His Arg Leu Asn Gly Pro Leu Lys Cys Gly Gln Pro
 465 470 475 480
 Gln Glu Val Leu Val Asp Tyr Tyr Ile Asp Pro Ala Asp Ala Ser Pro
 485 490 495
 Asp Gln Glu Ile Ser Phe Ser Tyr Tyr Leu Ile Gly Lys Gly Ser Leu
 500 505 510
 Val Met Glu Gly Gln Lys His Leu Asn Ser Lys Lys Lys Gly Leu Lys
 515 520 525
 Ala Ser Phe Ser Leu Ser Leu Thr Phe Thr Ser Arg Leu Ala Pro Asp
 530 535 540
 Pro Ser Leu Val Ile Tyr Ala Ile Phe Pro Ser Gly Gly Val Val Ala
 545 550 555 560
 Asp Lys Ile Gln Phe Ser Val Glu Met Cys Phe Asp Asn Gln Gln Leu
 565 570 575
 Pro Gly Ala Glu Val Glu Leu Gln Leu Gln Ala Ala Pro Gly Ser Leu
 580 585 590
 Cys Ala Leu Arg Ala Val Asp Glu Ser Val Leu Leu Leu Arg Pro Asp
 595 600 605
 Arg Glu Leu Ser Asn Arg Ser Val Tyr Gly Met Phe Pro Phe Trp Tyr
 610 615 620
 Gly His Tyr Pro Tyr Gln Val Ala Glu Tyr Asp Gln Cys Pro Val Ser
 625 630 635 640
 Gly Pro Trp Asp Phe Pro Gln Pro Leu Ile Asp Pro Met Pro Gln Gly
 645 650 655
 His Ser Ser Gln Arg Ser Ile Ile Trp Arg Pro Ser Phe Ser Glu Gly
 660 665 670
 Thr Asp Leu Phe Ser Phe Phe Arg Asp Val Gly Leu Lys Ile Leu Ser
 675 680 685
 Asn Ala Lys Ile Lys Lys Pro Val Asp Cys Ser His Arg Ser Pro Glu
 690 695 700

Tyr Ser Thr Ala Met Gly Gly Gly Gly His Pro Glu Ala Phe Glu Ser
705 710 715 720
Ser Thr Pro Leu His Gln Ala Glu Asp Ser Gln Val Arg Gln Tyr Phe
725 730 735
Pro Glu Thr Trp Leu Trp Asp Leu Phe Pro Ile Gly Asn Ser Gly Lys
740 745 750
Glu Ala Val His Val Thr Val Pro Asp Ala Ile Thr Glu Trp Lys Ala
755 760 765
Met Ser Phe Cys Thr Ser Gln Ser Arg Gly Phe Gly Leu Ser Pro Thr
770 775 780
Val Gly Leu Thr Ala Phe Lys Pro Phe Phe Val Asp Leu Thr Leu Pro
785 790 795 800
Tyr Ser Val Val Arg Gly Glu Ser Phe Arg Leu Thr Ala Thr Ile Phe
805 810 815
Asn Tyr Leu Lys Asp Cys Ile Arg Val Gln Thr Asp Leu Ala Lys Ser
820 825 830
His Glu Tyr Gln Leu Glu Ser Trp Ala Asp Ser Gln Thr Ser Ser Cys
835 840 845
Leu Cys Ala Asp Asp Ala Lys Thr His His Trp Asn Ile Thr Ala Val
850 855 860
Lys Leu Gly His Ile Asn Phe Thr Ile Ser Thr Lys Ile Leu Asp Ser
865 870 875 880
Asn Glu Pro Cys Gly Gly Gln Lys Gly Phe Val Pro Gln Lys Gly Arg
885 890 895
Ser Asp Thr Leu Ile Lys Pro Val Leu Val Lys Pro Glu Gly Val Leu
900 905 910
Val Glu Lys Thr His Ser Ser Leu Leu Cys Pro Lys Gly Gly Lys Val
915 920 925
Ala Ser Glu Ser Val Ser Leu Glu Leu Pro Val Asp Ile Val Pro Asp
930 935 940
Ser Thr Lys Ala Tyr Val Thr Val Leu Gly Asp Ile Met Gly Thr Ala
945 950 955 960
Leu Gln Asn Leu Asp Gly Leu Val Gln Met Pro Ser Gly Cys Gly Glu
965 970 975
Gln Asn Met Val Leu Phe Ala Pro Ile Ile Tyr Val Leu Gln Tyr Leu
980 985 990
Glu Lys Ala Gly Leu Leu Thr Glu Glu Ile Arg Ser Arg Ala Val Gly
995 1000 1005

Phe Leu Glu Ile Gly Tyr Gln Lys Glu Leu Met Tyr Lys His Ser Asn
1010 1015 1020
Gly Ser Tyr Ser Ala Phe Gly Glu Arg Asp Gly Asn Gly Asn Thr Trp
1025 1030 1035 1040
Leu Thr Ala Phe Val Thr Lys Cys Phe Gly Gln Ala Gln Lys Phe Ile
1045 1050 1055
Phe Ile Asp Pro Lys Asn Ile Gln Asp Ala Leu Lys Trp Met Ala Gly
1060 1065 1070
Asn Gln Leu Pro Ser Gly Cys Tyr Ala Asn Val Gly Asn Leu Leu His
1075 1080 1085
Thr Ala Met Lys Gly Gly Val Asp Asp Glu Val Ser Leu Thr Ala Tyr
1090 1095 1100
Val Thr Ala Ala Leu Leu Glu Met Gly Lys Asp Val Asp Asp Pro Met
1105 1110 1115 1120
Val Ser Gln Gly Leu Arg Cys Leu Lys Asn Ser Ala Thr Ser Thr Thr
1125 1130 1135
Asn Leu Tyr Thr Gln Ala Leu Leu Ala Tyr Ile Phe Ser Leu Ala Gly
1140 1145 1150
Glu Met Asp Ile Arg Asn Ile Leu Leu Lys Gln Leu Asp Gln Gln Ala
1155 1160 1165
Ile Ile Ser Gly Glu Ser Ile Tyr Trp Ser Gln Lys Pro Thr Pro Ser
1170 1175 1180
Ser Asn Ala Ser Pro Trp Ser Glu Pro Ala Ala Val Asp Val Glu Leu
1185 1190 1195 1200
Thr Ala Tyr Ala Leu Leu Ala Gln Leu Thr Lys Pro Ser Leu Thr Gln
1205 1210 1215
Lys Glu Ile Ala Lys Ala Thr Ser Ile Val Ala Trp Leu Ala Lys Gln
1220 1225 1230
His Asn Ala Tyr Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala
1235 1240 1245
Leu Gln Ala Leu Ala Lys Tyr Ala Thr Thr Ala Tyr Met Pro Ser Glu
1250 1255 1260
Glu Ile Asn Leu Val Val Lys Ser Thr Glu Asn Phe Gln Arg Thr Phe
1265 1270 1275 1280
Asn Ile Gln Ser Val Asn Arg Leu Val Phe Gln Gln Asp Thr Leu Pro
1285 1290 1295
Asn Val Pro Gly Met Tyr Thr Leu Glu Ala Ser Gly Gln Gly Cys Val
1300 1305 1310

Tyr Val Gln Thr Val Leu Arg Tyr Asn Ile Leu Pro Pro Thr Asn Met
 1315 1320 1325
 Lys Thr Phe Ser Leu Ser Val Glu Ile Gly Lys Ala Arg Cys Glu Gln
 1330 1335 1340
 Pro Thr Ser Pro Arg Ser Leu Thr Leu Thr Ile His Thr Ser Tyr Val
 1345 1350 1355 1360
 Gly Ser Arg Ser Ser Ser Asn Met Ala Ile Val Glu Val Lys Met Leu
 1365 1370 1375
 Ser Gly Phe Ser Pro Met Glu Gly Thr Asn Gln Leu Leu Leu Gln Gln
 1380 1385 1390
 Pro Leu Val Lys Lys Val Glu Phe Gly Thr Asp Thr Leu Asn Ile Tyr
 1395 1400 1405
 Leu Asp Glu Leu Ile Lys Asn Thr Gln Thr Tyr Thr Phe Thr Ile Ser
 1410 1415 1420
 Gln Ser Val Leu Val Thr Asn Leu Lys Pro Ala Thr Ile Lys Val Tyr
 1425 1430 1435 1440
 Asp Tyr Tyr Leu Pro Gly Ser Phe Lys Leu Ser Gln Tyr Thr Ile Val
 1445 1450 1455
 Trp Ser Met Asn Asn Asp Ser Ile Val Asp Ser Val Ala Arg His Pro
 1460 1465 1470
 Glu Pro Pro Pro Phe Lys Thr Glu Ala Phe Ile Pro Ser Leu Pro Gly
 1475 1480 1485
 Ser Val Asn Asn
 1490

<210> 11
 <211> 987
 <212> DNA
 <213> Homo sapiens

<400> 11
 atgagagcca attgttccag cagctcagcc tgccctgcca acagttcaga ggaggagctg 60
 ccagtgggac tggaggtgca tggaaacctg gagctcgttt tcacagtggg gtccactatc 120
 atgatggggc tgctcatgtt ctctttggga tgttccgtgg agatccggaa gctgtgggtcg 180
 cacatcagga gaccctgggg cattgctgtg ggactgctct gccagtttgg gctcatgcct 240
 tttacagctt atctcctggc cattagcttt tctctgaagc cagtccaagc tattgctgtt 300
 ctcatcatgg gctgctgccg gggggcacca tctetaacat tttcaccttc tgggttgatg 360
 gagatatgga tctcaggtgc cctgggaatg atgccactct gcatttatct ctacacctgg 420
 tcttgagtc ttcagcagaa tctcaccatt ccttatcaga acataggtct gtcttttagga 480
 attacccttg tgtgctgac cattcctgtg gcctttgggtg tctatgtgaa ttacagatgg 540
 ccaaaacaat ccaaaatcat tctcaaggcc gttgttgggtg gggtcctcct tctggtgggtc 600
 gcagttgctg gtgtggtcct ggcgaaagga tcttggaatt cagacatcac ccttctgacc 660
 atcagtttca tctttccttt gattggccat gtcacgggtt ttctgctggc actttttacc 720
 caccagtctt ggcaaaggac cttgcctatc tttttagggt tagctttcaa gacaccctgt 780
 gataccctac tcgcaatgac ttcgtgtcct gaatgttcca ggctcatcta tgccttcatt 840

cctctgctat atggactctt ccagctgata gatggatttc ttattgttga agagagaaca 900
gaagatacag actgcgatgg ttcaccttta cctgagtatt ttactgaggt aacaataata 960
cctaaacaac ctaggatatg acagctt 987

<210> 12
<211> 326
<212> PRT
<213> Homo sapiens

<400> 12

Met	Arg	Ala	Asn	Cys	Ser	Ser	Ser	Ser	Ala	Cys	Pro	Ala	Asn	Ser	Ser	1	5	10	15
Glu	Glu	Glu	Leu	Pro	Val	Gly	Leu	Glu	Val	His	Gly	Asn	Leu	Glu	Leu	20	25	30	
Val	Phe	Thr	Val	Val	Ser	Thr	Ile	Met	Met	Gly	Leu	Leu	Met	Phe	Ser	35	40	45	
Leu	Gly	Cys	Ser	Val	Glu	Ile	Arg	Lys	Leu	Trp	Ser	His	Ile	Arg	Arg	50	55	60	
Pro	Trp	Gly	Ile	Ala	Val	Gly	Leu	Leu	Cys	Gln	Phe	Gly	Leu	Met	Pro	65	70	75	80
Phe	Thr	Ala	Tyr	Leu	Leu	Ala	Ile	Ser	Phe	Ser	Leu	Lys	Pro	Val	Gln	85	90	95	
Ala	Ile	Ala	Val	Leu	Ile	Met	Gly	Cys	Cys	Arg	Gly	Ala	Pro	Ser	Leu	100	105	110	
Thr	Phe	Ser	Pro	Ser	Gly	Leu	Met	Glu	Ile	Trp	Ile	Ser	Gly	Ala	Leu	115	120	125	
Gly	Met	Met	Pro	Leu	Cys	Ile	Tyr	Leu	Tyr	Thr	Trp	Ser	Trp	Ser	Leu	130	135	140	
Gln	Gln	Asn	Leu	Thr	Ile	Pro	Tyr	Gln	Asn	Ile	Gly	Leu	Ser	Leu	Gly	145	150	155	160
Ile	Thr	Leu	Val	Cys	Leu	Thr	Ile	Pro	Val	Ala	Phe	Gly	Val	Tyr	Val	165	170	175	
Asn	Tyr	Arg	Trp	Pro	Lys	Gln	Ser	Lys	Ile	Ile	Leu	Lys	Ala	Val	Val	180	185	190	
Gly	Gly	Val	Leu	Leu	Leu	Val	Val	Ala	Val	Ala	Gly	Val	Val	Leu	Ala	195	200	205	
Lys	Gly	Ser	Trp	Asn	Ser	Asp	Ile	Thr	Leu	Leu	Thr	Ile	Ser	Phe	Ile	210	215	220	
Phe	Pro	Leu	Ile	Gly	His	Val	Thr	Gly	Phe	Leu	Leu	Ala	Leu	Phe	Thr	225	230	235	240
His	Gln	Ser	Trp	Gln	Arg	Thr	Leu	Pro	Ile	Phe	Leu	Gly	Leu	Ala	Phe				

245								250				255					
Lys	Thr	Pro	Cys	Asp	Thr	Leu	Leu	Ala	Met	Thr	Ser	Cys	Pro	Glu	Cys		
260								265				270					
Ser	Arg	Leu	Ile	Tyr	Ala	Phe	Ile	Pro	Leu	Leu	Tyr	Gly	Leu	Phe	Gln		
275								280				285					
Leu	Ile	Asp	Gly	Phe	Leu	Ile	Val	Glu	Glu	Arg	Thr	Glu	Asp	Thr	Asp		
290								295				300					
Cys	Asp	Gly	Ser	Pro	Leu	Pro	Glu	Tyr	Phe	Thr	Glu	Val	Thr	Ile	Ile		
305								310				315				320	
Pro	Lys	Gln	Pro	Arg	Ile												
325																	

50					55					60					
Ile	Ile	Phe	Asp	Cys	Arg	Ser	Gln	Pro	Arg	Asn	Val	Pro	Val	Ile	Thr
65					70					75					80
Gly	Ser	Lys	Asp	Leu	Gln	Asn	Val	Asn	Leu	Thr	Leu	Arg	Ile	Ile	Phe
				85					90					95	
Arg	Pro	Val	Ala	Ser	Gln	Leu	Pro	His	Ile	Phe	Thr	Ser	Ser	Gly	Glu
			100					105					110		
Asp	His	Asp	Glu	Arg	Val	Pro	Pro	Ser	Ile	Thr	Asn	Lys	Ile	Leu	Lys
		115					120					125			
Ser	Val	Val	Ala	Arg	Phe	Glu	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Arg	Glu
	130					135					140				
Gln	Ile	Ser	Arg	Gln	Val	Ser	Asp	Asp	Leu	Thr	Glu	Pro	Ala	Ala	Thr
145				150					155						160
Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	Tyr	Leu	Thr	Phe	Gly
			165						170					175	
Lys	Glu	Phe	Ile	Glu	Ala	Val	Glu	Ala	Lys	Gln	Ile	Ala	Gln	Gln	Glu
		180						185					190		
Ala	Glu	Arg	Ala	Arg	Phe	Val	Val	Glu	Lys	Ala	Glu	Gln	Gln	Lys	Lys
		195					200					205			
Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Val	Ala	Glu	Leu	Ile
	210					215					220				
Thr	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Ala	Leu	Ile	Glu	Leu	Arg	Lys
225				230						235					240
Leu	Glu	Ala	Val	Glu	Asp	Ile	Thr	Tyr	Gln	Leu	Leu	Arg	Ser	Arg	Asn
			245						250					255	
Ile	Thr	Tyr	Leu	Arg	Ala	Gly	Gln	Ser	Met	Pro	Leu	Gln	Leu	Arg	Trp
			260					265					270		

<210> 15
 <211> 2011
 <212> DNA
 <213> Homo sapiens

<400> 15
 atggggtggc tcccactcct gctgcttctg actcaatgct taggggtccc tggtcagcgc 60
 tcgccattga atgacttcca agtgctccgg ggcacagagc tacagcacct gctacatgcg 120
 gtgggtgccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc tggtcgctgt 180
 gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg ttgccaactg 240
 ctgccatgga ctcaacactc gccccacacg aggtgcggc gttctggggc ctgtgacctc 300
 ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg gtaccggggc 360

```

accatggcca cgaccgtggg tggcctgccc tgccaggett ggagccacaa gttcccaaatt 420
gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg ccgtaaccct 480
gatggcgacc cgggaggtcc ctggtgctac acaacagacc ctgctgtgcg cttccagagc 540
tgcggcacatca aatcctgccc ggaggccgcg tgtgtctggt gcaatggcga ggaataccgc 600
ggcgcggttag accgcacgga gtcagggcgc gactgcccagc gctgggatct tcagcaccgc 660
caccagcacc ccttcgagcc gggcaagtcc ctcgaccaag gtctggacga caactattgc 720
cggaatcctg acggctccga gcggccatgg tgctacacta cggatccgca gatcgagcga 780
gagttctgtg acctccccg ctgcggttcc gaggcacagc cccgccaaga ggccacaact 840
gtcagctgct tccgcgggaa ggggtgagggc taccggggca cagccaatac caccaccgcg 900
ggcgtacctt gccagcgttg ggacgcgcaa atcccgcatc agcaccgatt tacgccagaa 960
aaatacgctg gcaaggacct tcgggagaac ttctgccgga accccgacgg ctgagaggcg 1020
ccctggtgct tcacactgcg gcccggcatg cgcgcggcct tttgctacca gatccggcgt 1080
tgtacagacg acgtgcggcc ccagactgct accacggcgc aggggagcag taccgcggca 1140
cggtcagcaa gaccgcgaag ggtgtccagt gccagcgtg gtccgctgag acgccgcaca 1200
agccgcagtt cacgtttacc tccgaaccgc atgcacaact ggaggagaac ttctgccgga 1260
accagatgg ggatagccat gggccctggt gctacacgat ggaccaagg accccattcg 1320
actactgtgc cctgcgacgc tgcgctgatg accagccgcc atcaatcctg gacccccag 1380
accaggtgca gtttgagaag tgtggcaaga ggggtgatcg gctggatcag cggcgttcca 1440
agctgcgcgt ggttgggggc catccgggca actcaccctg gacagtcagc ttgcggaatc 1500
ggtatgctgc ctctcacggg ctatgaggta tggttgggca ccctgttcca gaaccacag 1560
catggagagc caagcctaca gcgggtccca gtagccaaga tgggtgtgtg gccctcaggc 1620
tcccagcttg tcctgctcaa gctggagaga tctgtgacct tgaaccagcg tgtggccctg 1680
atctgcctgc cccctgaatg gtatgtggtg cctccaggga ccaagtgtga gattgcaggc 1740
tggggtgaga ccaaaggtac gggtaatgac acagtccctaa atgtggcctt gctgaatgtc 1800
atctccaacc aggagtgtaa catcaagcac cgaggacgtg gtgactacgg gggcccactt 1860
gcctgcttta cccacaactg ctgggtcctg gaaggaatta taatcccaa ccgagtatgc 1920
gcaaggtcct gctggccagc tgtcttcacg cgtgtctctg tgtttgtgga ctggattcac 1980
aaggtcatga gactgggtta ggccagcct t 2011

```

<210> 16
 <211> 666
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
 1 5 10 15
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
 20 25 30
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
 85 90 95
 Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110

Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly	
		115					120					125				
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr	
	130					135					140					
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	
145					150					155					160	
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	
				165					170					175		
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	
		180						185					190			
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	
	195						200					205				
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	
	210					215					220					
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	
225					230					235					240	
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	
				245					250					255		
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	
		260						265					270			
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	
		275					280					285				
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	
	290					295					300					
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	
305					310					315					320	
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	
				325					330					335		
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	
			340					345					350			
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	
		355					360					365				
Thr	Ala	Thr	Thr	Ala	Gln	Gly	Ser	Ser	Thr	Ala	Ala	Arg	Ser	Ala	Arg	
	370					375					380					
Pro	Ala	Arg	Val	Ser	Ser	Ala	Ser	Ala	Gly	Pro	Leu	Arg	Arg	Arg	Thr	
385					390					395					400	
Ser	Arg	Ser	Ser	Arg	Leu	Pro	Pro	Asn	Arg	Met	His	Asn	Trp	Arg	Arg	
				405					410					415		

Thr Ser Ala Gly Thr Gln Met Gly Ile Ala Met Gly Pro Gly Ala Thr
 420 425 430
 Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala Ala
 435 440 445
 Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys Ser
 450 455 460
 Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Gly Val Pro
 465 470 475 480
 Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln Ser
 485 490 495
 Ala Cys Gly Ile Gly Met Leu Pro Leu Thr Gly Tyr Glu Val Trp Leu
 500 505 510
 Gly Thr Leu Phe Gln Asn Pro Gln His Gly Glu Pro Ser Leu Gln Arg
 515 520 525
 Val Pro Val Ala Lys Met Val Cys Gly Pro Ser Gly Ser Gln Leu Val
 530 535 540
 Leu Leu Lys Leu Glu Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu
 545 550 555 560
 Ile Cys Leu Pro Pro Glu Trp Tyr Val Val Pro Pro Gly Thr Lys Cys
 565 570 575
 Glu Ile Ala Gly Trp Gly Glu Thr Lys Gly Thr Gly Asn Asp Thr Val
 580 585 590
 Leu Asn Val Ala Leu Leu Asn Val Ile Ser Asn Gln Glu Cys Asn Ile
 595 600 605
 Lys His Arg Gly Arg Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr
 610 615 620
 His Asn Cys Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys
 625 630 635 640
 Ala Arg Ser Cys Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val
 645 650 655
 Asp Trp Ile His Lys Val Met Arg Leu Gly
 660 665

<210> 17

<211> 634

<212> DNA

<213> Homo sapiens

<400> 17

caagctgccc acgccgacgg caaccctgct ctgcatgccc gcccgcccgt gccaccatg 60
 gccacagttc agcagctggg aggaagatgg cgcctggtgg acagcaaacg ctttgatgaa 120

tacatgaagg agggaggagt ggggaactgct ttgcgaaaaa tggacgcaat ggccaagcca 180
gattgtatca tcacttgtga tggcaaaaac ctcaccataa aaaccgagag cactttgaaa 240
acacagtttt cttgtaccct gggagagaag tttgaagaaa ccacagctga tggcagaaaa 300
actcagactg tgtgcagctt tgcagatggt gcattgggttc agcatcagga gtgggatggg 360
aaggaaaaca caataacaag aaaactgaaa gatgggaaat tagtggtgta ctgtgtcatg 420
aacaatgtcg cctgtactcg gatctatgaa aaagtagaat aaaaattcca tcatcacttt 480
ggacaggagt taactaatag aatgatcaag ctcagttcaa tgagcaaadc tccatagtgt 540
tttttttcat tactgtgttc aattatcttt atcacaaacg tttcacatgc agctatttca 600
aagtgtcttg gattaattag gatcatccct ttgg 634

<210> 18
<211> 134
<212> PRT
<213> Homo sapiens

<400> 18
Met Ala Thr Val Gln Gln Leu Gly Gly Arg Trp Arg Leu Val Asp Ser
1 5 10 15
Lys Arg Phe Asp Glu Tyr Met Lys Glu Gly Gly Val Gly Thr Ala Leu
20 25 30
Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
35 40 45
Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe
50 55 60
Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg
65 70 75 80
Lys Thr Gln Thr Val Cys Ser Phe Ala Asp Gly Ala Leu Val Gln His
85 90 95
Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp
100 105 110
Gly Lys Leu Val Val Tyr Cys Val Met Asn Asn Val Ala Cys Thr Arg
115 120 125
Ile Tyr Glu Lys Val Glu
130

<210> 19
<211> 822
<212> DNA
<213> Homo sapiens

<400> 19
catgaactgg gcatttctgc agggcctgct gaggggcgtg aacaagtact ccacagtgct 60
gagccgcatc tggctgtctg tgggtgttcat ctttcgtgtg ctgggtgtacg tgggtggcagc 120
ggaggagggtg tgggacgatg agcagaagga ctttgtctgc aacaccaagc agcccggtg 180
ccccaacgtc tgctatgacg agttcttccc cgtgtcccac gtgcgcctct gggccctaca 240
gctcatcctg gtcacgtgcc cctcactgct cgtgggtcatg cacgtggcct accgcgagga 300
acgcgagcgc aagcaccacc tgaaacacgg gcccaatgcc ccgtccctgt acgacaacct 360


```

gagcaagaag cggggcggac tgtggtggac gtacttgctg agcctcatct tcaaggccgc 420
cgtggatgct ggcttcctct atatcttcca ccgcctctac aaggattatg acatgccccg 480
cgtggtggcc tgctcctggg agccttgccc ccacactgtg gactgttaca tctcccggcc 540
cacggagaag aaggtcttca cctacttcat ggtgaccaca gctgccatct gcatcctgct 600
caacctcagt gaagtcttct acctggtggg caagaggtgc atggagatct tcggccccag 660
gcaccggcgg cctcggtgcc gggaatgcct acccgatacg tgcccacat atgtcctctc 720
ccagggaggg caccctgagg atgggaactc tgtcctaata aaggctgggt cggccccagt 780
ggatgcaggt gggatatccat aacctgcgag atcagcagat aa 822

```

<210> 20
 <211> 266
 <212> PRT
 <213> Homo sapiens

```

<400> 20
Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
  1                      5                      10                      15

Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
          20                      25                      30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
      35                      40                      45

Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
      50                      55                      60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
      65                      70                      75                      80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
          85                      90                      95

Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
      100                      105                      110

Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
      115                      120                      125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
      130                      135                      140

Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
      145                      150                      155                      160

Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
          165                      170                      175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
          180                      185                      190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
          195                      200                      205

Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
      210                      215                      220

```

Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
 225 230 235 240

Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
 245 250 255

Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
 260 265

<210> 21
 <211> 546
 <212> DNA
 <213> Homo sapiens

<400> 21
 caatctgaca tgtaactgta aaatcactgg gcccgaggag tgactgtaat taagggctta 60
 cgttgaaaat gtataaacag agcttgattc ttaagtttcg aaaattcttc acagtgatgg 120
 tgtgaactaa atccacagcc acataataat caaaacagaa aagcaaaaga aagccacttc 180
 aggaaatacc acggtcacac ctcagttggc ttcattgctac agattataga aaatatgttg 240
 ctgcccgggc caccaatctg ttggttcaca ttactacgtg agcaatgtaa gtgtttgcaa 300
 gaagccatcc actatctaaa tatcagatat agatgctcca aagcagctac gtcagtgatg 360
 agaacagaga aaatacgtag caacatttca ttaagttgaa ttctaatact taaaaggctc 420
 ctttttagtac tgacattctg gatttttaaaa gttatgttga cgcgatgttc tctactcaca 480
 gtgggagttg aacaatgaga acacacggac acggggaagg gaacatcaca caccagggcc 540
 tgtcag 546

<210> 22
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Leu Gln Ile Ile Glu Asn Met Leu Leu Pro Gly Pro Pro Ile Cys
 1 5 10 15

Trp Phe Thr Leu Leu Arg Glu Gln Cys Lys Cys Leu Gln Glu Ala Ile
 20 25 30

His Tyr Leu Asn Ile Arg Tyr Arg Cys Ser Lys Ala Ala Thr Ser Val
 35 40 45

Met Arg Thr Glu Lys Ile Arg Ser Asn Ile Ser Leu Ser
 50 55 60

<210> 23
 <211> 2309
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (2196)
 <223> Wherein n is an a o t o r c o r g.

<400> 23

```
gagtgaagagg tcggacagac tgtggagccg acagactgaa ggacagcggc accgccagac 60
ggccagaaag ttccgccatg agctggggca cggagctgtg ggatcagttc gacagcttag 120
acaagcatac acaatgggga attgacttct tggaaagata tgccaaattt gttaaagaga 180
ggatagaaat tgaacagaac tatgcgaaac aattgagaaa tctggttaag aagtactgcc 240
ccaaacgttc atccaaagat gaagagccac ggtttacctc gtgtgtagcc tttttaata 300
tccttaatga gttaaagac tatgcaggac agcgagaagt tgtagcagaa gaaatggcgc 360
acagagtgtg tgggtgaatta atgagatatg ctcgatctct gaaaactgaa agaaaaatgc 420
atctgcaaga aggacgaaaa gctcaacaat atcttgacat gtgctggaaa cagatgggta 480
atagtaaaaa gaagtttgaa agagaatgta gagaggcaga aaaggcacia cagagttagt 540
aaagattgga taatgatact aatgcaacca aggcagatgt tgaaaatgcc aaacagcagt 600
tgaatctgcg tacgcatatg gccgatgaaa ataaaaatgc atatgctgca caattacaaa 660
actttaatgg agaacaacat aaacattttt atgtagtgtg tcctcagatt tacaagcaac 720
tacaagaaat ggacgaacga aggactatta aactcagtga gtgttacaga ggatttgctg 780
actcagaacg caaagttatt cccatcattt caaaatgttt ggaaggaatg attcttgctg 840
caaaatcagt tgatgaaaga agagactctc aaatgggtgt agactccttc aaatctgggt 900
ttgaacctcc aggagacttt ccatttgaag attacagtca acatatatat agaaccattt 960
ctgatgggac tatcagtgtc tccaaacagg agagtgggaa gatggatgcc aaaaccccag 1020
taggaaaggc caagggcaaa ttgtggctct ttggaaagaa gccaaagggc ccagcactag 1080
aagatttcag tcatctgcca ccagaacaga gacgtaaaaa actacagcag cgcattgatg 1140
aacttaacag agaactacag aaagaatcag accaaaaaga tgcactcaac aaaatgaaag 1200
atgtatatga gaaggatcca caaatggggg atccagggag ttgacagcct aaattagcag 1260
agaccatgaa taacattgac cgcctacgaa tggaaatcca taagaatgag gcttggctct 1320
ctgaagtcga aggcaaaaca ggtgggagag gagacagaag acatagcagt gacataaatc 1380
atcttghtaa acagggacga gaaagtcctg agggaagtta cactgatgat gcaaaccagg 1440
aagtcctgtg gccacccag cagcatggtc accacaatga gtttgatgat gaatttgagg 1500
atgatgatcc ctgtcctgct attggacact gcaaagctat ctaccctttt gatggacata 1560
atgaaggtac tctagcaatg aaagaagggt aagttctcta cattatagag gaggacaaag 1620
gtgacggatg gacaagagct cggagacaga acggtgaaga aggtctacgt cccacgtcat 1680
acatagatgt aactctagag aaaaacagta aaggttctct aagaggggtt ctgaggaaat 1740
gggcaagatg ttgaaggagg ttacatgcag ctgcttttgg gggaggggtat tagagtgtgc 1800
aggctcaaag agagtgtgag aagcaagttg catgagtgtc tgcagacatg attttttttt 1860
tactaacttc attagcattt ccatacattg tttttaaaaa tcataatacc aacccttaag 1920
ttcctagttc acagttatcc ccacaaaaga aaaagccaac aatagtgtac catttttcta 1980
ttttatttta ttgctgtcta atcaataaag aatgcagagc tgtcaaaaaa tgtgtcttac 2040
atntagctgt cccaacagga ttgtcttccc tcccagctct ggttttaatt ggcttttaga 2100
cccactatct gtcagatcct tgccatctgt cagtgtctgc ctgcgccacc tccgtgcttg 2160
cctaacatcc tgttgcatgt ctagegtgat tgagcnagat ttccaggcat gtcttttagaa 2220
tcccctggtg ctgtcaaagc ctggtttggg ttacattggg ngtgcaatcn ctttgtcaac 2280
atctccagca ctatngttcc ntcttaggt 2309
```

<210> 24

<211> 547

<212> PRT

<213> Homo sapiens

<400> 24

```
Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Ser Leu Asp Lys
  1             5             10             15
```

```
His Thr Gln Trp Gly Ile Asp Phe Leu Glu Arg Tyr Ala Lys Phe Val
      20             25             30
```

```
Lys Glu Arg Ile Glu Ile Glu Gln Asn Tyr Ala Lys Gln Leu Arg Asn
    35             40             45
```

Leu	Val	Lys	Lys	Tyr	Cys	Pro	Lys	Arg	Ser	Ser	Lys	Asp	Glu	Glu	Pro	50	55	60	
Arg	Phe	Thr	Ser	Cys	Val	Ala	Phe	Phe	Asn	Ile	Leu	Asn	Glu	Leu	Asn	65	70	75	80
Asp	Tyr	Ala	Gly	Gln	Arg	Glu	Val	Val	Ala	Glu	Glu	Met	Ala	His	Arg	85	90	95	
Val	Tyr	Gly	Glu	Leu	Met	Arg	Tyr	Ala	His	Asp	Leu	Lys	Thr	Glu	Arg	100	105	110	
Lys	Met	His	Leu	Gln	Glu	Gly	Arg	Lys	Ala	Gln	Gln	Tyr	Leu	Asp	Met	115	120	125	
Cys	Trp	Lys	Gln	Met	Gly	Asn	Ser	Lys	Lys	Lys	Phe	Glu	Arg	Glu	Cys	130	135	140	
Arg	Glu	Ala	Glu	Lys	Ala	Gln	Gln	Ser	Tyr	Glu	Arg	Leu	Asp	Asn	Asp	145	150	155	160
Thr	Asn	Ala	Thr	Lys	Ala	Asp	Val	Glu	Asn	Ala	Lys	Gln	Gln	Leu	Asn	165	170	175	
Leu	Arg	Thr	His	Met	Ala	Asp	Glu	Asn	Lys	Asn	Ala	Tyr	Ala	Ala	Gln	180	185	190	
Leu	Gln	Asn	Phe	Asn	Gly	Glu	Gln	His	Lys	His	Phe	Tyr	Val	Val	Ile	195	200	205	
Pro	Gln	Ile	Tyr	Lys	Gln	Leu	Gln	Glu	Met	Asp	Glu	Arg	Arg	Thr	Ile	210	215	220	
Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe	Ala	Asp	Ser	Glu	Arg	Lys	Val	225	230	235	240
Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu	Gly	Met	Ile	Leu	Ala	Ala	Lys	245	250	255	
Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln	Met	Val	Val	Asp	Ser	Phe	Lys	260	265	270	
Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	Pro	Phe	Glu	Asp	Tyr	Ser	Gln	275	280	285	
His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly	Thr	Ile	Ser	Ala	Ser	Lys	Gln	290	295	300	
Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	Pro	Val	Gly	Lys	Ala	Lys	Gly	305	310	315	320
Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	Lys	Gly	Pro	Ala	Leu	Glu	Asp	325	330	335	
Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg	340	345	350	

Ile Asp Glu Leu Asn Arg Glu Leu Gln Lys Glu Ser Asp Gln Lys Asp
 355 360 365
 Ala Leu Asn Lys Met Lys Asp Val Tyr Glu Lys Asp Pro Gln Met Gly
 370 375 380
 Asp Pro Gly Ser Leu Gln Pro Lys Leu Ala Glu Thr Met Asn Asn Ile
 385 390 395 400
 Asp Arg Leu Arg Met Glu Ile His Lys Asn Glu Ala Trp Leu Ser Glu
 405 410 415
 Val Glu Gly Lys Thr Gly Gly Arg Gly Asp Arg Arg His Ser Ser Asp
 420 425 430
 Ile Asn His Leu Val Thr Gln Gly Arg Glu Ser Pro Glu Gly Ser Tyr
 435 440 445
 Thr Asp Asp Ala Asn Gln Glu Val Arg Gly Pro Pro Gln Gln His Gly
 450 455 460
 His His Asn Glu Phe Asp Asp Glu Phe Glu Asp Asp Asp Pro Leu Pro
 465 470 475 480
 Ala Ile Gly His Cys Lys Ala Ile Tyr Pro Phe Asp Gly His Asn Glu
 485 490 495
 Gly Thr Leu Ala Met Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu
 500 505 510
 Asp Lys Gly Asp Gly Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu
 515 520 525
 Gly Tyr Val Pro Thr Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser
 530 535 540
 Lys Gly Ser
 545

<210> 25
 <211> 1787
 <212> DNA
 <213> Homo sapiens

<400> 25
 gcggaacatt gcctagtaga ccctgaggct ttacaacagt gccactgacc cctatgagcc 60
 tgatgctgga tgaccaaccc cctatggagg cccagtatgc agaggagggc ccaggacctg 120
 ggatcttcag agcagagcct ggagaccagc agcatcccat ttctcaggcg gtgtgctggc 180
 gttccatgcg acgtggctgt gcagtgctgg gagccctggg gctgctggcc ggtgcagggtg 240
 ttggctcatg gctcctagtg ctgtatctgt gtccctgctgc ctctcagccc atttccggga 300
 ccttgacagga tgaggagata actttgagct gctcagaggc cagcgctgag gaagctctgc 360
 tccctgcact tcccaaaaca gtatctttca gaataaacag cgaagacttc ttgctggaag 420
 cgcaagtgcg ggatcagcca cgctggctcc tggctctgcca tgagggctgg agccccgccc 480
 tggggctgca gatctgctgg agccttgggc atctcagact cactcaccac aagggagtaa 540
 acctcactga catcaaactc aacagttccc aggagtattgc tcagctctct cctagactgg 600

gaggcttcct	ggaggaggcg	tggcagccca	gtaggactac	tgaggctgtt	aggaacaact	660
gcacttctgg	tcaagttgtt	tccctcagat	gctctgagtg	tggagcgagg	cccctggctt	720
cccggatagt	tgggtgggag	tctgtggctc	ctgggcgctg	gccgtggcag	gccagcgtgg	780
ccctgggctt	ccggcacacg	tgtgggggct	ctgtgctagc	gccacgctgg	gtggtgactg	840
ctgcacattg	tatgcacagt	ttcaggctgg	cccgcctgtc	cagctggcgg	gttcatgcgg	900
ggctgggtcag	ccacagtgcc	gtcaggcccc	accaaggggc	tctggtggag	aggattatcc	960
cacacccctt	ctacagtgcc	cagaatcatg	actacgacgt	cgccctcctg	aggctccaga	1020
ccgctctcaa	cttctcagac	actgtgggcg	ctgtgtgcct	gccggccaag	gaacagcatt	1080
ttccgaaggg	ctcgcggtgc	tgggtgtctg	gctggggcca	caccaccctt	agccatactt	1140
acagctcgga	tatgctccga	gacacggtgg	tgccctgctt	cagcactcag	ctctgcaaca	1200
gctcttgctg	gtacagcgga	gccctcaccg	cccgcctgct	ttgcgctggc	tacctggacg	1260
gaagggctga	tgcattgccag	ggagatagcg	ggggccccct	agtgtgcccc	gatggggaca	1320
catggcgctt	agtgggggtg	gtcagctggg	ggcgtggctg	cgcagagccc	aatcaccag	1380
gtgtctacgc	caaggtagct	gagtttctgg	actggatcca	tgacactgct	caggtgagtg	1440
tgggggcagg	agtagggcag	ggagatttct	aaaggacctg	ccctcgaatg	caaggaacct	1500
taccccttag	gccccggccc	tgctggggac	tggggagggt	gctaggacat	attccccaga	1560
gtgagtggag	gaagaagtga	agcttaaaca	tggaaatccat	tggatttcta	tcagtttaag	1620
gatgaactgg	gtaagagtat	gcctgagttt	gtatcccaga	tctaccattt	cctgtgtcga	1680
cctttggcaa	atttctaact	ttgttaaacc	ttaatttcct	gataataacc	atgatggcta	1740
cttatatgct	attgttatat	gctattaaat	aagaccgcta	caatgcc		1787

<210> 26

<211> 1787

<212> DNA

<213> Homo sapiens

<400> 26

ggcattgtac	gggtcttatt	taatagcata	taacaatagc	atataagtag	ccatcatggt	60
tattatcagg	aaattaaggt	ttaacaaagt	tagaaatttg	ccaaaggctg	acacaggaaa	120
tggtagatct	gggatacaaa	ctcaggcata	ctcttaccga	gttcatcctt	aaactgatag	180
aaatccaatg	gattccatgt	ttaagcttca	cttcttcttc	cactcactct	ggggaatatg	240
tcctagcacc	ctccccagtc	cccagcaggg	cccgggccta	aggggtaagg	ttccttgcat	300
tcgagggcag	gtcctttaga	aatctccctg	ccctactcct	gccccacac	tcacctgagc	360
agtgtcatgg	atccagtcca	gaaactcagc	taccttggcg	tagacacctg	ggtgattggg	420
ctctgcgcag	ccacgcccc	agctgaccac	cccactagg	cgccatgtgt	ccccatctgg	480
gcacactagg	gggccccgcg	tatctccctg	gcatgcatca	gcccttccgt	ccaggtagcc	540
agcgaaaagc	atgcgggggg	tgagggtcc	gctgtacacg	caagagctgt	tgcagagctg	600
agtgtctgagc	aggggcacca	ccgtgtcctg	gagcatatcc	gagctgtaag	tatggctagg	660
gtgggtgtgg	ccccagccag	acaccagca	ccgcgagccc	ttcgaaaat	gctgttcctt	720
ggccggcagg	cacacagcgc	ccacagtgtc	tgagaagttg	agagcggctt	ggagcctcag	780
gagggcgacg	tcgtagtcat	gattctgggc	actgtagagg	gggtgtggga	taatcctctc	840
caccagagcc	ccttgggtggg	gcctgacggc	actgtggctg	accagccccg	catgaacccg	900
ccagctggac	aggcgggcca	gcctgaaact	gtgcatacaa	tgtgcagcag	tcaccacca	960
gcgtggcgct	agcacagagc	ccccacacgt	gtgccggaag	cccagggcca	cgctggcctg	1020
ccacggccag	cgcccaggag	ccacagactg	cccaccaact	atccgggaag	ccaggggcct	1080
cgctccacac	tcagagcatc	tgagggaac	aacttgacca	gaagtgcagt	tggttcctaac	1140
agcctcagta	gtcctactgg	gctgccacgc	ctcctccagg	aagcctccca	gtctaggaga	1200
gagctgagca	aactcctggg	aactgttag	tttgatgtca	gtgaggttta	ctcccttggtg	1260
gtgagttagt	ctgagatgcc	caaggctcca	gcagatctgc	agccccaggg	cggggctcca	1320
gccctcatgg	cagaccagga	gccagcgtgg	ctgatccctc	acttgcgctt	ccagcaagaa	1380
gtcttcgctg	tttattctga	aagatactgt	tttggggaagt	gcaggagca	gagcttcctc	1440
agcgtggcc	tctgagcagc	tcaaagttat	ctcctcatcc	tgcaagggtcc	cggaaatggg	1500
ctgagaggca	gcaggacaca	gatacagcac	taggagccat	gagccaacac	ctgcaccggc	1560
cagcagcccc	agggctccca	gcactgcaca	gccacgtcgc	atggaacgcc	agcacaccgc	1620
ctgagaaatg	ggatgctgct	ggtctccagg	ctctgctctg	aagatcccag	gtcctggggc	1680
ctcctctgca	tactgggcct	ccataggggg	ttggtcatcc	agcatcaggc	tcataggggt	1740

cagtggcact gttgtaaagc ctcaggtct actaggcaat gttccgc

1787

<210> 27

<211> 472

<212> PRT

<213> Homo sapiens

<400> 27

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
1 5 10 15

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
20 25 30

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
35 40 45

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
50 55 60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
65 70 75 80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
85 90 95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
100 105 110

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln
115 120 125

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
130 135 140

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
145 150 155 160

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
165 170 175

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
180 185 190

Ser Arg Thr Thr Glu Ala Val Arg Asn Asn Cys Thr Ser Gly Gln Val
195 200 205

Val Ser Leu Arg Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg
210 215 220

Ile Val Gly Gly Gln Ser Val Ala Pro Gly Arg Trp Pro Trp Gln Ala
225 230 235 240

Ser Val Ala Leu Gly Phe Arg His Thr Cys Gly Gly Ser Val Leu Ala
245 250 255

Pro Arg Trp Val Val Thr Ala Ala His Cys Met His Ser Phe Arg Leu
 260 265 270
 Ala Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Ser
 275 280 285
 Ala Val Arg Pro His Gln Gly Ala Leu Val Glu Arg Ile Ile Pro His
 290 295 300
 Pro Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Arg
 305 310 315 320
 Leu Gln Thr Ala Leu Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu
 325 330 335
 Pro Ala Lys Glu Gln His Phe Pro Lys Gly Ser Arg Cys Trp Val Ser
 340 345 350
 Gly Trp Gly His Thr His Pro Ser His Thr Tyr Ser Ser Asp Met Leu
 355 360 365
 Gln Asp Thr Val Val Pro Leu Leu Ser Thr Gln Leu Cys Asn Ser Ser
 370 375 380
 Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala Gly Tyr
 385 390 395 400
 Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu
 405 410 415
 Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val Ser Trp
 420 425 430
 Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala Lys Val
 435 440 445
 Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Val Ser Val Gly
 450 455 460
 Ala Gly Val Gly Gln Gly Asp Phe
 465 470

<210> 28

<211> 2148

<212> DNA

<213> Homo sapiens

<400> 28

acgcgggata cagggagggg ccatgtgcga accagggaga cctcatcttc caaccaagct 60
 tgctgggctt gcatttaatc aatgcatggc cagagaacag gagcggaaca ttgcctagta 120
 gaccctgagg ctttacaaca gtgctactga cccctatgag cctgatgctg gatgaccaac 180
 cccctatgga ggcccagtat gcagaggagg gcccaggacc tgggatcttc agagcagagc 240
 ctggagacca gcagcatccc atttctcagg cggtgtgctg gcgttccatg cgacgtggct 300
 gtgcagtgtc gggagccctg gggctgctgg ccggtgcagg tgttggtca tggctcctag 360
 tgctgtatct gtgtcctgct gcctctcagc ccatttccgg gaccttgcag gatgaggaga 420
 taactttgag ctgctcagag gccagcgtg aggaagctct gctccctgca ctccccaaaa 480


```

cagtatcttt cagaataaac agcgaagact tcttgctgga agcgaagtg agggatcagc 540
cacgctggct cctggtctgc catgagggtt ggagccccgc cctggggctg cagatctgct 600
ggagccttgg gcatctcaga ctactcacc acaagggagt aaacctcact gacatcaaac 660
tcaacagttc ccaggagttt gctcagctct ctccctagact gggagggttc ctggaggagg 720
cgtggcagcc caggaacaac tgcacttctg gtcaagttgt ttccctcaga tgctctgagt 780
gtggagcgag gccccctggc tcccggatag ttggtgggca gtctgtggct cctgggctgt 840
ggccgtggca ggccagcgtg gccctgggct tccggcacac gtgtgggggc tctgtgctag 900
cgccacgctg ggtggtgact gctgcacatt gtatgcacag tgcccagaat catgactacg 960
acgtcgccct cctgaggctc cagaccgctc tcaacttctc agacactgtg ggcgctgtgt 1020
gacctgccgg caaggaacag ctttttccga agggctcgcg gtgctgggtg tccggctggt 1080
gccacaccca cctagccat acttacagct cggatatgct ccaggacacg gtggtgcccc 1140
tgctcagcac tcagctctgc aacagctctt gcgtgtacag cggagccctc accccccgca 1200
tgctttgcgc tggctacctg gacggaaggg ctgatgcatg ccaggagatg agcggggggc 1260
ccctagtgtg ccagatggg gacacatggc gcctagtggg ggtggtcagc tgggggctgt 1320
gctgctcaga gcccacac ccagggtgtc acgccaaggt agctgagttt ctggactgga 1380
tccatgacac tgctcaggac tccctcctct gactcctgct gtttctctca gtctcactgc 1440
acaccactgc ctcatgttc ctggggcctc cagcagctcc actaatggag gagaggcagt 1500
agcctccgac acagaacgca tggacctct actactgtgt gtgaggaaca gtcactacc 1560
actggccagc caccagcca acaggtctct cctcttgggc cctgatttca gactcctct 1620
tctcactaga gactcaatga cagaagagag gctgggactt ggttgggcat gctgtggtt 1680
ctgaggggatg agggggagga gagaggtagg agctggagat gaagagactg ctagaagcag 1740
caggaagcct gcccttctgc cctctccct cctgccccct gtgtgagtct tttaggagg 1800
gtgactggga ggtgcccccc gtcccacctt tttcctgtgc tctaggtggg ctaagtgcct 1860
ccctagagga ctccatggc gagaggctcc tgggcagatg ggttcaaggc tgggcccagtc 1920
ccagatgaag cctatgggag tcaggacctc ctccactctc cctctccact ccccttctct 1980
ttctcacctg gctgtggctg gccctgtgtg ggggtgggtac actggaaaac aagaaggtt 2040
gagttggtct aggacattgg ttttaaata cagttctgtg aactggtcca aggaggttct 2100
gttattaaag tgatatatgg tcttgaaaaa aaaaaaaaaa aaaaaaaa 2148

```

<210> 29
 <211> 418
 <212> PRT
 <213> Homo sapiens

```

<400> 29
Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1             5             10             15

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
      20             25             30

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
      35             40             45

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
      50             55             60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
      65             70             75             80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
      85             90             95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
      100             105             110

```

Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln		
		115					120					125					
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly		
		130				135					140						
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys		
145					150					155					160		
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala		
				165					170					175			
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro		
			180					185						190			
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu		
		195					200					205					
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val		
	210					215					220						
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg		
225					230					235					240		
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala		
				245					250					255			
Ala	His	Cys	Met	His	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu		
			260					265					270				
Leu	Arg	Leu	Gln	Thr	Ala	Leu	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val		
		275					280					285					
Cys	Leu	Pro	Ala	Lys	Glu	Gln	His	Phe	Pro	Lys	Gly	Ser	Arg	Cys	Trp		
	290					295					300						
Val	Ser	Gly	Trp	Cys	His	Thr	His	Pro	Ser	His	Thr	Tyr	Ser	Ser	Asp		
305					310					315					320		
Met	Leu	Gln	Asp	Thr	Val	Val	Pro	Leu	Leu	Ser	Thr	Gln	Leu	Cys	Asn		
				325					330					335			
Ser	Ser	Cys	Val	Tyr	Ser	Gly	Ala	Leu	Thr	Pro	Arg	Met	Leu	Cys	Ala		
			340					345					350				
Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly		
		355					360					365					
Pro	Leu	Val	Cys	Pro	Asp	Gly	Asp	Thr	Trp	Arg	Leu	Val	Gly	Val	Val		
		370				375					380						
Ser	Trp	Gly	Arg	Gly	Cys	Ala	Glu	Pro	Asn	His	Pro	Gly	Val	Tyr	Ala		
385					390					395					400		
Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile	His	Asp	Thr	Ala	Gln	Asp	Ser		
				405					410					415			

Leu Leu

<210> 30

<211> 1593

<212> PRT

<213> Homo sapiens

<400> 30

Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala
1 5 10 15

Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro
20 25 30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly
35 40 45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly
50 55 60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg
65 70 75 80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser
85 90 95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe
100 105 110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His
115 120 125

Val Lys Met Met Ala Ser Ser Ala Pro Leu Cys His Leu Ser Gly Thr
130 135 140

Val Leu Gln Gln Gly Thr Arg Val Gly Thr Ala Ala Leu Ser Ala Cys
145 150 155 160

His Gly Leu Thr Gly Phe Phe Gln Leu Pro His Gly Asp Phe Phe Ile
165 170 175

Glu Pro Val Lys Lys His Pro Leu Val Glu Gly Gly Tyr His Pro His
180 185 190

Ile Val Tyr Arg Arg Gln Lys Val Pro Glu Thr Lys Glu Pro Thr Cys
195 200 205

Gly Leu Lys Asp Ser Val Asn Ile Ser Gln Lys Gln Glu Leu Trp Arg
210 215 220

Glu Lys Trp Glu Arg His Asn Leu Pro Ser Arg Ser Leu Ser Arg Arg
225 230 235 240

Ser Ile Ser Lys Glu Arg Trp Val Glu Thr Leu Val Val Ala Asp Thr
245 250 255

Lys	Met	Ile	Glu	Tyr	His	Gly	Ser	Glu	Asn	Val	Glu	Ser	Tyr	Ile	Leu	260	265	270
Thr	Ile	Met	Asn	Met	Val	Thr	Gly	Leu	Phe	His	Asn	Pro	Ser	Ile	Gly	275	280	285
Asn	Ala	Ile	His	Ile	Val	Val	Val	Arg	Leu	Ile	Leu	Leu	Glu	Glu	Glu	290	295	300
Glu	Gln	Gly	Leu	Lys	Ile	Val	His	His	Ala	Glu	Lys	Thr	Leu	Ser	Ser	305	310	315
Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Asn	Pro	Lys	Ser	Asp	Leu	Asn	Pro	325	330	335
Val	His	His	Asp	Val	Ala	Val	Leu	Leu	Thr	Arg	Lys	Asp	Ile	Cys	Ala	340	345	350
Gly	Phe	Asn	Arg	Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Leu	Ser	Gly	355	360	365
Met	Cys	Gln	Pro	His	Arg	Ser	Cys	Asn	Ile	Asn	Glu	Asp	Ser	Gly	Leu	370	375	380
Pro	Leu	Ala	Phe	Thr	Ile	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	385	390	395
Gln	His	Asp	Gly	Lys	Glu	Asn	Asp	Cys	Glu	Pro	Val	Gly	Arg	His	Pro	405	410	415
Tyr	Ile	Met	Ser	Arg	Gln	Leu	Gln	Tyr	Asp	Pro	Thr	Pro	Leu	Thr	Trp	420	425	430
Ser	Lys	Cys	Ser	Glu	Glu	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	435	440	445
Gly	Phe	Cys	Leu	Asp	Asp	Ile	Pro	Lys	Lys	Lys	Gly	Leu	Lys	Ser	Lys	450	455	460
Val	Ile	Ala	Pro	Gly	Val	Ile	Tyr	Asp	Val	His	His	Gln	Cys	Gln	Leu	465	470	475
Gln	Tyr	Gly	Pro	Asn	Ala	Thr	Phe	Cys	Gln	Glu	Val	Glu	Asn	Val	Cys	485	490	495
Gln	Thr	Leu	Trp	Cys	Ser	Val	Lys	Gly	Phe	Cys	Arg	Ser	Lys	Leu	Asp	500	505	510
Ala	Ala	Ala	Asp	Gly	Thr	Gln	Cys	Gly	Glu	Lys	Lys	Trp	Cys	Met	Ala	515	520	525
Gly	Lys	Cys	Ile	Thr	Val	Gly	Lys	Lys	Pro	Glu	Ser	Ile	Pro	Gly	Gly	530	535	540
Trp	Gly	Arg	Trp	Ser	Pro	Trp	Ser	His	Cys	Ser	Arg	Thr	Cys	Gly	Ala	545	550	555

Gly	Val	Gln	Ser	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Pro	Glu	Pro	Lys	Phe	
				565					570					575		
Gly	Gly	Lys	Tyr	Cys	Thr	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Leu	Cys	Asn	
			580					585					590			
Val	His	Pro	Cys	Arg	Ser	Glu	Ala	Pro	Thr	Phe	Arg	Gln	Met	Gln	Cys	
		595					600					605				
Ser	Glu	Phe	Asp	Thr	Val	Pro	Tyr	Lys	Asn	Glu	Leu	Tyr	His	Trp	Phe	
	610					615					620					
Pro	Ile	Phe	Asn	Pro	Ala	His	Pro	Cys	Glu	Leu	Tyr	Cys	Arg	Pro	Ile	
625					630					635					640	
Asp	Gly	Gln	Phe	Ser	Glu	Lys	Met	Leu	Asp	Ala	Val	Ile	Asp	Gly	Thr	
				645					650					655		
Pro	Cys	Phe	Glu	Gly	Gly	Asn	Ser	Arg	Asn	Val	Cys	Ile	Asn	Gly	Ile	
			660					665					670			
Cys	Lys	Met	Val	Gly	Cys	Asp	Tyr	Glu	Ile	Asp	Ser	Asn	Ala	Thr	Glu	
		675					680					685				
Asp	Arg	Cys	Gly	Val	Cys	Leu	Gly	Asp	Gly	Ser	Ser	Cys	Gln	Thr	Val	
	690					695					700					
Arg	Lys	Met	Phe	Lys	Gln	Lys	Glu	Gly	Ser	Gly	Tyr	Val	Asp	Ile	Gly	
705					710					715					720	
Leu	Ile	Pro	Lys	Gly	Ala	Arg	Asp	Ile	Arg	Val	Met	Glu	Ile	Glu	Gly	
				725					730					735		
Ala	Gly	Asn	Phe	Leu	Ala	Ile	Arg	Ser	Glu	Asp	Pro	Glu	Lys	Tyr	Tyr	
			740					745					750			
Leu	Asn	Gly	Gly	Phe	Ile	Ile	Gln	Trp	Asn	Gly	Asn	Tyr	Lys	Leu	Ala	
		755					760					765				
Gly	Thr	Val	Phe	Gln	Tyr	Asp	Arg	Lys	Gly	Asp	Leu	Glu	Lys	Leu	Met	
	770					775					780					
Ala	Thr	Gly	Pro	Thr	Asn	Glu	Ser	Val	Trp	Ile	Gln	Leu	Leu	Phe	Gln	
785					790					795					800	
Val	Thr	Asn	Pro	Gly	Ile	Lys	Tyr	Glu	Tyr	Thr	Ile	Gln	Lys	Asp	Gly	
				805					810					815		
Leu	Asp	Asn	Asp	Val	Glu	Gln	Met	Tyr	Phe	Trp	Gln	Tyr	Gly	His	Trp	
			820					825					830			
Thr	Glu	Cys	Ser	Val	Thr	Cys	Gly	Thr	Gly	Ile	Arg	Arg	Gln	Thr	Ala	
		835					840					845				
His	Cys	Ile	Lys	Lys	Gly	Arg	Gly	Met	Val	Lys	Ala	Thr	Phe	Cys	Asp	
	850					855					860					

Pro Glu Thr Gln Pro Asn Gly Arg Gln Lys Lys Cys His Glu Lys Ala
 865 870 875 880
 Cys Pro Pro Arg Trp Trp Ala Gly Glu Trp Glu Ala Cys Ser Ala Thr
 885 890 895
 Cys Gly Pro His Gly Glu Lys Lys Arg Thr Val Leu Cys Ile Gln Thr
 900 905 910
 Met Val Ser Asp Glu Gln Ala Leu Pro Pro Thr Asp Cys Gln His Leu
 915 920 925
 Leu Lys Pro Lys Thr Leu Leu Ser Cys Asn Arg Asp Ile Leu Cys Pro
 930 935 940
 Ser Asp Trp Thr Val Gly Asn Trp Ser Glu Cys Ser Val Ser Cys Gly
 945 950 955 960
 Gly Gly Val Arg Ile Arg Ser Val Thr Cys Ala Lys Asn His Asp Glu
 965 970 975
 Pro Cys Asp Val Thr Arg Lys Pro Asn Ser Arg Ala Leu Cys Gly Leu
 980 985 990
 Gln Gln Cys Pro Ser Ser Arg Arg Val Leu Lys Pro Asn Lys Gly Thr
 995 1000 1005
 Ile Ser Asn Gly Lys Asn Pro Pro Thr Leu Lys Pro Val Pro Pro Pro
 1010 1015 1020
 Thr Ser Arg Pro Arg Met Leu Thr Thr Pro Thr Gly Pro Glu Ser Met
 1025 1030 1035 1040
 Ser Thr Ser Thr Pro Ala Ile Ser Ser Pro Ser Pro Thr Thr Ala Ser
 1045 1050 1055
 Lys Glu Gly Asp Leu Gly Gly Lys Gln Trp Gln Asp Ser Ser Thr Gln
 1060 1065 1070
 Pro Glu Leu Ser Ser Arg Tyr Leu Ile Ser Thr Gly Ser Thr Ser Gln
 1075 1080 1085
 Pro Ile Leu Thr Ser Gln Ser Leu Ser Ile Gln Pro Ser Glu Glu Asn
 1090 1095 1100
 Val Ser Ser Ser Asp Thr Gly Pro Thr Ser Glu Gly Gly Leu Val Ala
 1105 1110 1115 1120
 Thr Thr Thr Ser Gly Ser Gly Leu Ser Ser Ser Arg Asn Pro Ile Thr
 1125 1130 1135
 Trp Pro Val Thr Pro Phe Tyr Asn Thr Leu Thr Lys Gly Pro Glu Met
 1140 1145 1150
 Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys
 1155 1160 1165

Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn
 1170 1175 1180

Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr
 1185 1190 1195 1200

Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met
 1205 1210 1215

Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr
 1220 1225 1230

Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu Leu
 1235 1240 1245

Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr Ala Asn
 1250 1255 1260

Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr Lys Ser Ser
 1265 1270 1275 1280

Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu Ile Thr Glu Gly
 1285 1290 1295

Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu Thr Asn Gly His Gly
 1300 1305 1310

Ser Ala His Trp Ile Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys
 1315 1320 1325

Gly Leu Gly Ala Tyr Trp Lys Arg Val Glu Cys Thr Thr Gln Met Asp
 1330 1335 1340

Ser Asp Cys Ala Ala Ile Gln Arg Pro Asp Pro Ala Lys Arg Cys His
 1345 1350 1355 1360

Leu Arg Pro Cys Ala Gly Trp Lys Val Gly Asn Trp Ser Lys Cys Ser
 1365 1370 1375

Arg Asn Cys Ser Gly Gly Phe Lys Ile Arg Glu Ile Gln Cys Val Asp
 1380 1385 1390

Ser Arg Asp His Arg Asn Leu Arg Pro Phe His Cys Gln Phe Leu Ala
 1395 1400 1405

Gly Ile Pro Pro Pro Leu Ser Met Ser Cys Asn Pro Glu Pro Cys Glu
 1410 1415 1420

Ala Trp Gln Val Glu Pro Trp Ser Gln Cys Ser Arg Ser Cys Gly Gly
 1425 1430 1435 1440

Gly Val Gln Glu Arg Gly Val Phe Cys Pro Gly Gly Leu Cys Asp Trp
 1445 1450 1455

Thr Lys Arg Pro Thr Ser Thr Met Ser Cys Asn Glu His Leu Cys Cys
 1460 1465 1470

His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly
 1475 1480 1485
 Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys
 1490 1495 1500
 Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro
 1505 1510 1515 1520
 Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu
 1525 1530 1535
 Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys
 1540 1545 1550
 Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe
 1555 1560 1565
 Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln
 1570 1575 1580
 Arg Leu Leu Gln Lys Ser Lys Glu Leu
 1585 1590

<210> 31
 <211> 1077
 <212> PRT
 <213> Homo sapiens

<400> 31
 Arg Ser Gln Asp Glu Phe Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala
 1 5 10 15
 Phe Pro Thr Arg Val Asp His Asn Gly Ala Leu Leu Ala Phe Ser Pro
 20 25 30
 Pro Pro Pro Arg Arg Gln Arg Arg Gly Thr Gly Ala Thr Ala Glu Ser
 35 40 45
 Arg Leu Phe Tyr Lys Val Ala Ser Pro Ser Thr His Phe Leu Leu Asn
 50 55 60
 Leu Thr Arg Ser Ser Arg Leu Leu Ala Gly His Val Ser Val Glu Tyr
 65 70 75 80
 Trp Thr Arg Glu Gly Leu Ala Trp Gln Arg Ala Ala Arg Pro His Cys
 85 90 95
 Leu Tyr Ala Gly His Leu Gln Gly Gln Ala Ser Ser Ser His Val Ala
 100 105 110
 Ile Ser Thr Cys Gly Gly Leu His Gly Leu Ile Val Ala Asp Glu Glu
 115 120 125
 Glu Tyr Leu Ile Glu Pro Leu His Gly Gly Pro Lys Gly Ser Arg Ser

130					135					140					
Pro	Glu	Glu	Ser	Gly	Pro	His	Val	Val	Tyr	Lys	Arg	Ser	Ser	Leu	Arg
145					150					155					160
His	Pro	His	Leu	Asp	Thr	Ala	Cys	Gly	Val	Arg	Asp	Glu	Lys	Pro	Trp
			165						170					175	
Lys	Gly	Arg	Pro	Trp	Trp	Leu	Arg	Thr	Leu	Lys	Pro	Pro	Pro	Ala	Arg
			180					185						190	
Pro	Leu	Gly	Asn	Glu	Thr	Glu	Arg	Gly	Gln	Pro	Gly	Leu	Lys	Arg	Ser
		195					200					205			
Val	Ser	Arg	Glu	Arg	Tyr	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Lys	Met
	210					215					220				
Met	Val	Ala	Tyr	His	Gly	Arg	Arg	Asp	Val	Glu	Gln	Tyr	Val	Leu	Ala
225					230					235					240
Ile	Met	Asn	Ile	Val	Ala	Lys	Leu	Phe	Gln	Asp	Ser	Ser	Leu	Gly	Ser
			245						250					255	
Thr	Val	Asn	Ile	Leu	Val	Thr	Arg	Leu	Ile	Leu	Leu	Thr	Glu	Asp	Gln
			260					265					270		
Pro	Thr	Leu	Glu	Ile	Thr	His	His	Ala	Gly	Lys	Ser	Leu	Asp	Ser	Phe
		275					280					285			
Cys	Lys	Trp	Gln	Lys	Ser	Ile	Val	Asn	His	Ser	Gly	His	Gly	Asn	Ala
	290					295					300				
Ile	Pro	Glu	Asn	Gly	Val	Ala	Asn	His	Asp	Thr	Ala	Val	Leu	Ile	Thr
305					310					315					320
Arg	Tyr	Asp	Ile	Cys	Ile	Tyr	Lys	Asn	Lys	Pro	Cys	Gly	Thr	Leu	Gly
			325						330					335	
Leu	Ala	Pro	Val	Gly	Gly	Met	Cys	Glu	Arg	Glu	Arg	Ser	Cys	Ser	Val
			340					345					350		
Asn	Glu	Asp	Ile	Gly	Leu	Pro	Gln	Ala	Phe	Thr	Ile	Ala	His	Glu	Ile
		355					360					365			
Gly	His	Thr	Phe	Gly	Met	Asn	His	Asp	Gly	Val	Gly	Asn	Ser	Cys	Gly
	370					375					380				
Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	Met
385					390					395					400
Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Asn	Arg	Asp	Tyr	Ile	Thr
			405						410					415	
Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	Pro
			420					425					430		
Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	Asp

435					440					445					
Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	Cys
450					455					460					
Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	Asn
465					470					475					480
Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	Gln
				485					490					495	
Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	Pro
			500					505					510		
Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	Thr
			515				520					525			
Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	Ser
			530				535					540			
Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	Cys
545					550					555					560
Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	Pro
				565					570					575	
Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	Ser
			580					585					590		
Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	Gly
			595				600					605			
Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Ser	Leu	Ala	Glu	Gly	Phe	Asn	Phe
			610				615					620			
Tyr	Thr	Glu	Arg	Ala	Ala	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Arg	Pro
625					630					635					640
Asp	Thr	Val	Asp	Ile	Cys	Val	Ser	Gly	Glu	Cys	Lys	His	Val	Gly	Cys
				645					650					655	
Asp	Arg	Val	Leu	Gly	Ser	Asp	Leu	Arg	Glu	Asp	Lys	Cys	Arg	Val	Cys
			660					665					670		
Gly	Gly	Asp	Gly	Ser	Ala	Cys	Glu	Thr	Ile	Glu	Gly	Val	Phe	Ser	Pro
			675				680					685			
Ala	Ser	Pro	Gly	Ala	Gly	Tyr	Glu	Asp	Val	Val	Trp	Ile	Pro	Lys	Gly
			690				695					700			
Ser	Val	His	Ile	Phe	Ile	Gln	Asp	Leu	Asn	Leu	Ser	Leu	Ser	His	Leu
705					710					715					720
Ala	Leu	Lys	Gly	Asp	Gln	Glu	Ser	Leu	Leu	Leu	Glu	Gly	Leu	Pro	Gly
				725					730					735	
Thr	Pro	Gln	Pro	His	Arg	Leu	Pro	Leu	Ala	Gly	Thr	Thr	Phe	Gln	Leu

740						745						750					
Arg	Gln	Gly	Pro	Asp	Gln	Val	Gln	Ser	Leu	Glu	Ala	Leu	Gly	Pro	Ile		
755						760						765					
Asn	Ala	Ser	Leu	Ile	Val	Met	Val	Leu	Ala	Arg	Thr	Glu	Leu	Pro	Ala		
770						775						780					
Leu	Arg	Tyr	Arg	Phe	Asn	Ala	Pro	Ile	Ala	Arg	Asp	Ser	Leu	Pro	Pro		
785						790						795			800		
Tyr	Ser	Trp	His	Tyr	Ala	Pro	Trp	Thr	Lys	Cys	Ser	Ala	Gln	Cys	Ala		
			805						810						815		
Gly	Gly	Ser	Gln	Val	Gln	Ala	Val	Glu	Cys	Arg	Asn	Gln	Leu	Asp	Ser		
			820						825						830		
Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	Lys		
			835						840						845		
Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	Val		
			850						855						860		
Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	Ser		
865						870						875			880		
Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	Ala		
			885						890						895		
Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	Ala		
			900						905						910		
Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	Ser		
			915						920						925		
Glu	Cys	Thr	Pro	Ser	Cys	Gly	Pro	Gly	Leu	Arg	His	Arg	Val	Val	Leu		
930						935						940					
Cys	Lys	Ser	Ala	Asp	His	Arg	Ala	Thr	Leu	Pro	Pro	Ala	His	Cys	Ser		
945						950						955			960		
Pro	Ala	Ala	Lys	Pro	Pro	Ala	Thr	Met	Arg	Cys	Asn	Leu	Arg	Arg	Cys		
			965						970						975		
Pro	Pro	Ala	Arg	Trp	Val	Ala	Gly	Glu	Trp	Gly	Glu	Cys	Ser	Ala	Gln		
			980						985						990		
Cys	Gly	Val	Gly	Gln	Arg	Gln	Arg	Ser	Val	Arg	Cys	Thr	Ser	His	Thr		
995						1000						1005					
Gly	Gln	Ala	Ser	His	Glu	Cys	Thr	Glu	Ala	Leu	Arg	Pro	Pro	Thr	Thr		
1010						1015						1020					
Gln	Gln	Cys	Glu	Ala	Lys	Cys	Asp	Ser	Pro	Thr	Pro	Gly	Asp	Gly	Pro		
1025						1030						1035			1040		
Glu	Glu	Cys	Lys	Asp	Val	Asn	Lys	Val	Ala	Tyr	Cys	Pro	Leu	Val	Leu		

	1045		1050		1055
Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys					
	1060		1065		1070
Thr Cys Gln Gly His					
	1075				
<210> 32					
<211> 997					
<212> PRT					
<213> Homo sapiens					
<400> 32					
Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro					
1		5		10	15
Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala					
	20		25		30
Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro					
	35		40		45
Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro					
	50		55		60
Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala					
	65		70		75
Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr					
	85		90		95
Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg					
	100		105		110
Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys					
	115		120		125
His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala					
	130		135		140
Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn					
	145		150		155
Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly					
	165		170		175
His Ala Gln Pro His Val Val Tyr Lys Arg Gln Ala Pro Glu Arg Leu					
	180		185		190
Ala Gln Arg Gly Asp Ser Ser Ala Pro Ser Thr Cys Gly Val Gln Val					
	195		200		205
Tyr Pro Glu Leu Glu Ser Arg Arg Glu Arg Trp Glu Gln Arg Gln Gln					
	210		215		220

Trp Arg Arg Pro Arg Leu Arg Arg Leu His Gln Arg Ser Val Ser Lys
 225 230 235 240
 Glu Lys Trp Val Glu Thr Leu Val Val Ala Asp Ala Lys Met Val Glu
 245 250 255
 Tyr His Gly Gln Pro Gln Val Glu Ser Tyr Val Leu Thr Ile Met Asn
 260 265 270
 Met Val Ala Gly Leu Phe His Asp Pro Ser Ile Gly Asn Pro Ile His
 275 280 285
 Ile Thr Ile Val Arg Leu Val Leu Leu Glu Asp Glu Glu Glu Asp Leu
 290 295 300
 Lys Ile Thr His His Ala Asp Asn Thr Leu Lys Ser Phe Cys Lys Trp
 305 310 315 320
 Gln Lys Ser Ile Asn Met Lys Gly Asp Ala His Pro Leu His His Asp
 325 330 335
 Thr Ala Ile Leu Leu Thr Arg Lys Asp Leu Cys Ala Ala Met Asn Arg
 340 345 350
 Pro Cys Glu Thr Leu Gly Leu Ser His Val Ala Gly Met Cys Gln Pro
 355 360 365
 His Arg Ser Cys Ser Ile Asn Glu Asp Thr Gly Leu Pro Leu Ala Phe
 370 375 380
 Thr Val Ala His Glu Leu Gly His Ser Phe Gly Ile Gln His Asp Gly
 385 390 395 400
 Ser Gly Asn Asp Cys Glu Pro Val Gly Lys Arg Pro Phe Ile Met Ser
 405 410 415
 Pro Gln Leu Leu Tyr Asp Ala Ala Pro Leu Thr Trp Ser Arg Cys Ser
 420 425 430
 Arg Gln Tyr Ile Thr Arg Phe Leu Asp Arg Gly Trp Gly Leu Cys Leu
 435 440 445
 Asp Asp Pro Pro Ala Lys Asp Ile Ile Asp Phe Pro Ser Val Pro Pro
 450 455 460
 Gly Val Leu Tyr Asp Val Ser His Gln Cys Arg Leu Gln Tyr Gly Ala
 465 470 475 480
 Tyr Ser Ala Phe Cys Glu Asp Met Asp Asn Val Cys His Thr Leu Trp
 485 490 495
 Cys Ser Val Gly Thr Thr Cys His Ser Lys Leu Asp Ala Ala Val Asp
 500 505 510
 Gly Thr Arg Cys Gly Glu Asn Lys Trp Cys Leu Ser Gly Glu Cys Val
 515 520 525

Pro Val Gly Phe Arg Pro Glu Ala Val Asp Gly Gly Trp Ser Gly Trp
 530 535 540
 Ser Ala Trp Ser Ile Cys Ser Arg Ser Cys Gly Met Gly Val Gln Ser
 545 550 555 560
 Ala Glu Arg Gln Cys Thr Gln Pro Thr Pro Lys Tyr Lys Gly Arg Tyr
 565 570 575
 Cys Val Gly Glu Arg Lys Arg Phe Arg Leu Cys Asn Leu Gln Ala Cys
 580 585 590
 Pro Ala Gly Arg Pro Ser Phe Arg His Val Gln Cys Ser His Phe Asp
 595 600 605
 Ala Met Leu Tyr Lys Gly Gln Leu His Thr Trp Val Pro Val Val Asn
 610 615 620
 Asp Val Asn Pro Cys Glu Leu His Cys Arg Pro Ala Asn Glu Tyr Phe
 625 630 635 640
 Ala Lys Lys Leu Arg Asp Ala Val Val Asp Gly Thr Pro Cys Tyr Gln
 645 650 655
 Val Arg Ala Ser Arg Asp Leu Cys Ile Asn Gly Ile Cys Lys Asn Val
 660 665 670
 Gly Cys Asp Phe Glu Ile Asp Ser Gly Ala Met Glu Asp Arg Cys Gly
 675 680 685
 Val Cys His Gly Asn Gly Ser Thr Cys His Thr Val Ser Gly Thr Phe
 690 695 700
 Glu Glu Ala Glu Gly Leu Gly Tyr Val Asp Val Gly Leu Ile Pro Ala
 705 710 715 720
 Gly Ala Arg Glu Ile Arg Ile Gln Glu Val Ala Glu Ala Ala Asn Phe
 725 730 735
 Leu Ala Leu Arg Ser Glu Asp Pro Glu Lys Tyr Phe Leu Asn Gly Gly
 740 745 750
 Trp Thr Ile Gln Trp Asn Gly Asp Tyr Gln Val Ala Gly Thr Thr Phe
 755 760 765
 Thr Tyr Ala Arg Arg Gly Asn Trp Glu Asn Leu Thr Ser Pro Gly Pro
 770 775 780
 Thr Lys Glu Pro Val Trp Ile Gln Val Pro Ala Ser Arg Gly Pro Gly
 785 790 795 800
 Gly Gly Ser Arg Gly Gly Val Pro Arg Pro Ser Thr Leu His Gly Arg
 805 810 815
 Ser Arg Pro Gly Gly Val Ser Pro Gly Ser Val Thr Glu Pro Gly Ser
 820 825 830

Glu Pro Gly Pro Pro Ala Ala Ala Ser Thr Ser Val Ser Pro Ser Leu
 835 840 845
 Lys Trp Pro Asn Leu Val Ala Ala Val His Arg Gly Gly Trp Gly Gln
 850 855 860
 Ala Pro Leu Gly Leu Gly Gly Trp Arg Arg His Leu Val Leu Met Gly
 865 870 875 880
 Pro Arg Leu Pro Thr Gln Leu Leu Phe Gln Glu Ser Asn Pro Gly Val
 885 890 895
 His Tyr Glu Tyr Thr Ile His Arg Glu Ala Gly Gly His Asp Glu Val
 900 905 910
 Pro Pro Pro Val Phe Ser Trp His Tyr Gly Pro Trp Thr Lys Cys Thr
 915 920 925
 Val Thr Cys Gly Arg Gly Glu Lys Trp Gly Arg His Ser Pro Thr Cys
 930 935 940
 Arg Gly Leu Val Ser Gly Gln Gly His Trp Leu Gln Leu Pro Ala His
 945 950 955 960
 Cys Trp Ala Thr Thr Gly Leu Glu Val Cys Phe Ser Glu Pro Gln Phe
 965 970 975
 Ser Ile Cys Glu Met Arg Leu Ala Ile Ala Leu Cys Pro Arg Pro Ala
 980 985 990
 Gly Arg Val His Gly
 995

<210> 33
 <211> 854
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu
 1 5 10 15
 Ala Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly
 20 25 30
 Ser Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp
 35 40 45
 Gln Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser
 50 55 60
 Phe Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn
 65 70 75 80
 Ala Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile
 85 90 95

Thr	Arg	Tyr	Asp	Ile	Cys	Ile	Tyr	Lys	Asn	Lys	Pro	Cys	Gly	Thr	Leu	100	105	110
Gly	Leu	Ala	Pro	Val	Gly	Gly	Met	Cys	Glu	Arg	Glu	Arg	Ser	Cys	Ser	115	120	125
Val	Asn	Glu	Asp	Ile	Gly	Leu	Ala	Thr	Ala	Phe	Thr	Ile	Ala	His	Glu	130	135	140
Ile	Gly	His	Thr	Phe	Gly	Met	Asn	His	Asp	Gly	Val	Gly	Asn	Ser	Cys	145	150	155
Gly	Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	165	170	175
Met	Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Ser	Arg	Asp	Tyr	Ile	180	185	190
Thr	Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	195	200	205
Pro	Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	210	215	220
Asp	Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	225	230	235
Cys	Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	245	250	255
Asn	Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	260	265	270
Gln	Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	275	280	285
Pro	Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	290	295	300
Thr	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	305	310	315
Ser	Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	325	330	335
Cys	Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	340	345	350
Pro	Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	355	360	365
Ser	Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	370	375	380
Gly	Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Cys	Leu	Ala	Glu	Gly	Phe	Asn	385	390	395
																		400

Phe Tyr Thr Glu Arg Ala Ala Ala Val Val Asp Gly Thr Pro Cys Arg
405 410 415
Pro Asp Thr Val Asp Ile Cys Val Ser Gly Glu Cys Lys His Val Gly
420 425 430
Cys Asp Arg Val Leu Gly Ser Asp Leu Arg Glu Asp Lys Cys Arg Val
435 440 445
Cys Gly Gly Asp Gly Ser Ala Cys Glu Thr Ile Glu Gly Val Phe Ser
450 455 460
Pro Ala Ser Pro Gly Ala Gly Tyr Glu Asp Val Val Trp Ile Pro Lys
465 470 475 480
Gly Ser Val His Ile Phe Ile Gln Asp Leu Asn Leu Ser Leu Ser His
485 490 495
Leu Ala Leu Lys Gly Asp Gln Glu Ser Leu Leu Leu Glu Gly Leu Pro
500 505 510
Gly Thr Pro Gln Pro His Arg Leu Pro Leu Ala Gly Thr Thr Phe Gln
515 520 525
Leu Arg Gln Gly Pro Asp Gln Val Gln Ser Leu Glu Ala Leu Gly Pro
530 535 540
Ile Asn Ala Ser Leu Ile Val Met Val Leu Ala Arg Thr Glu Leu Pro
545 550 555 560
Ala Leu Arg Tyr Arg Phe Asn Ala Pro Ile Ala Arg Asp Ser Leu Pro
565 570 575
Pro Tyr Ser Trp His Tyr Ala Pro Trp Thr Lys Cys Ser Ala Gln Cys
580 585 590
Ala Gly Gly Ser Gln Val Gln Ala Val Glu Cys Arg Asn Gln Leu Asp
595 600 605
Ser Ser Ala Val Ala Pro His Tyr Cys Ser Ala His Ser Lys Leu Pro
610 615 620
Lys Arg Gln Arg Ala Cys Asn Thr Glu Pro Cys Pro Pro Asp Trp Val
625 630 635 640
Val Gly Asn Trp Ser Leu Cys Ser Arg Ser Cys Asp Ala Gly Val Arg
645 650 655
Ser Arg Ser Val Val Cys Gln Arg Arg Val Ser Ala Ala Glu Glu Lys
660 665 670
Ala Leu Asp Asp Ser Ala Cys Pro Gln Pro Arg Pro Pro Val Leu Glu
675 680 685
Ala Cys His Gly Pro Thr Cys Pro Pro Glu Trp Ala Ala Leu Asp Trp
690 695 700

Ser Glu Cys Thr Pro Ser Cys Gly Pro Gly Leu Arg His Arg Val Val
 705 710 715 720
 Leu Cys Lys Ser Ala Asp His Arg Ala Thr Leu Pro Pro Ala His Cys
 725 730 735
 Ser Pro Ala Ala Lys Pro Pro Ala Thr Met Arg Cys Asn Leu Arg Arg
 740 745 750
 Cys Pro Pro Ala Arg Trp Val Ala Gly Glu Trp Gly Glu Cys Ser Ala
 755 760 765
 Gln Cys Gly Val Gly Gln Arg Gln Arg Ser Val Arg Cys Thr Ser His
 770 775 780
 Thr Gly Gln Ala Ser His Glu Cys Thr Glu Ala Leu Arg Pro Pro Thr
 785 790 795 800
 Thr Gln Gln Cys Glu Ala Lys Cys Asp Ser Pro Thr Pro Gly Asp Gly
 805 810 815
 Pro Glu Glu Cys Lys Asp Val Asn Lys Val Ala Tyr Cys Pro Leu Val
 820 825 830
 Leu Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys
 835 840 845
 Lys Thr Cys His Gly His
 850

<210> 34
 <211> 860
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (450)
 <223> Wherein Xaa is any amino acid.

<400> 34
 Met Glu Ile Leu Trp Lys Thr Leu Thr Trp Ile Leu Ser Leu Ile Met
 1 5 10 15
 Ala Ser Ser Glu Phe His Ser Asp His Arg Leu Ser Tyr Ser Ser Gln
 20 25 30
 Glu Glu Phe Leu Thr Tyr Leu Glu His Tyr Gln Leu Thr Ile Pro Ile
 35 40 45
 Arg Val Asp Gln Asn Gly Ala Phe Leu Ser Phe Thr Val Lys Asn Asp
 50 55 60
 Lys His Ser Arg Arg Arg Arg Ser Met Asp Pro Ile Asp Pro Gln Gln
 65 70 75 80

Ala Val Ser Lys Leu Phe Phe Lys Leu Ser Ala Tyr Gly Lys His Phe
 85 90 95
 His Leu Asn Leu Thr Leu Asn Thr Asp Phe Val Ser Lys His Phe Thr
 100 105 110
 Val Glu Tyr Trp Gly Lys Asp Gly Pro Gln Trp Lys His Asp Phe Leu
 115 120 125
 Asp Asn Cys His Tyr Thr Gly Tyr Leu Gln Asp Gln Arg Ser Thr Thr
 130 135 140
 Lys Val Ala Leu Ser Asn Cys Val Gly Leu His Gly Val Ile Ala Thr
 145 150 155 160
 Glu Asp Glu Glu Tyr Phe Ile Glu Pro Leu Lys Asn Thr Thr Glu Asp
 165 170 175
 Ser Lys His Phe Ser Tyr Glu Asn Gly His Pro His Val Ile Tyr Lys
 180 185 190
 Lys Ser Ala Leu Gln Gln Arg His Leu Tyr Asp His Ser His Cys Gly
 195 200 205
 Val Ser Asp Phe Thr Arg Ser Gly Lys Pro Trp Trp Leu Asn Asp Thr
 210 215 220
 Ser Thr Val Ser Tyr Ser Leu Pro Ile Asn Asn Thr His Ile His His
 225 230 235 240
 Arg Gln Lys Arg Ser Val Ser Ile Glu Arg Phe Val Glu Thr Leu Val
 245 250 255
 Val Ala Asp Lys Met Met Val Gly Tyr His Gly Arg Lys Asp Ile Glu
 260 265 270
 His Tyr Ile Leu Ser Val Met Asn Ile Val Ala Lys Leu Tyr Arg Asp
 275 280 285
 Ser Ser Leu Gly Asn Val Val Asn Ile Ile Val Ala Arg Leu Ile Val
 290 295 300
 Leu Thr Glu Asp Gln Pro Asn Leu Glu Ile Asn His His Ala Asp Lys
 305 310 315 320
 Ser Leu Asp Ser Phe Cys Lys Trp Gln Lys Ser Ile Leu Ser His Gln
 325 330 335
 Ser Asp Gly Asn Thr Ile Pro Glu Asn Gly Ile Ala His His Asp Asn
 340 345 350
 Ala Val Leu Ile Thr Arg Tyr Asp Ile Cys Thr Tyr Lys Asn Lys Pro
 355 360 365
 Cys Gly Thr Leu Gly Leu Ala Ser Val Ala Gly Met Cys Glu Pro Glu
 370 375 380

Arg Ser Cys Ser Ile Asn Glu Asp Ile Gly Leu Gly Ser Ala Phe Thr
 385 390 395 400
 Ile Ala His Glu Ile Val His Asn Phe Gly Met Asn His Asp Gly Ile
 405 410 415
 Gly Asn Ser Cys Gly Arg Lys Val Met Lys Gln Gln Asn Tyr Gly Ser
 420 425 430
 Ser His Tyr Cys Glu Tyr Gln Ser Phe Phe Leu Val Cys Leu Gln Ser
 435 440 445
 Arg Xaa His His Gln Leu Phe Arg Glu Val Cys Arg Glu Leu Trp Cys
 450 455 460
 Leu Ser Lys Ser Asn Arg Cys Val Thr Asn Ser Ile Pro Ala Ala Glu
 465 470 475 480
 Gly Thr Leu Cys Gln Thr Gly Asn Ile Glu Lys Gly Trp Cys Tyr Gln
 485 490 495
 Gly Asp Cys Val Pro Phe Gly Thr Trp Pro Gln Ser Ile Asp Gly Gly
 500 505 510
 Trp Gly Pro Trp Ser Leu Trp Gly Glu Cys Ser Arg Thr Cys Gly Gly
 515 520 525
 Gly Val Ser Ser Ser Leu Arg His Cys Asp Ser Pro Ala Pro Ser Gly
 530 535 540
 Gly Gly Lys Tyr Cys Leu Gly Glu Arg Lys Arg Tyr Arg Ser Cys Asn
 545 550 555 560
 Thr Asp Pro Cys Pro Leu Gly Ser Arg Asp Phe Arg Glu Lys Gln Cys
 565 570 575
 Ala Asp Phe Asp Asn Met Pro Phe Arg Gly Lys Tyr Tyr Asn Trp Lys
 580 585 590
 Pro Tyr Thr Gly Gly Gly Val Lys Pro Cys Ala Leu Asn Cys Leu Ala
 595 600 605
 Glu Gly Tyr Asn Phe Tyr Thr Glu Arg Ala Pro Ala Val Ile Asp Gly
 610 615 620
 Thr Gln Cys Asn Ala Asp Ser Leu Asp Ile Cys Ile Asn Gly Glu Cys
 625 630 635 640
 Lys His Val Gly Cys Asp Asn Ile Leu Gly Ser Asp Ala Arg Glu Asp
 645 650 655
 Arg Cys Arg Val Cys Gly Gly Gly Gly Ser Thr Cys Asp Ala Ile Glu
 660 665 670
 Gly Phe Phe Asn Asp Ser Leu Pro Arg Gly Gly Tyr Met Glu Val Val
 675 680 685

Gln Ile Pro Arg Gly Ser Val His Ile Glu Val Arg Glu Val Ala Met
 690 695 700
 Ser Lys Asn Tyr Ile Ala Leu Lys Ser Glu Gly Asp Asp Tyr Tyr Ile
 705 710 715 720
 Asn Gly Ala Trp Thr Ile Asp Trp Pro Arg Lys Phe Asp Val Ala Gly
 725 730 735
 Thr Ala Phe His Tyr Lys Arg Pro Thr Asp Glu Pro Glu Ser Leu Glu
 740 745 750
 Ala Leu Gly Pro Thr Ser Glu Asn Leu Ile Val Met Val Leu Leu Gln
 755 760 765
 Glu Gln Asn Leu Gly Ile Arg Tyr Lys Phe Asn Val Pro Ile Thr Arg
 770 775 780
 Thr Gly Ser Gly Asp Asn Glu Val Gly Phe Thr Trp Asn His Gln Pro
 785 790 795 800
 Trp Ser Glu Cys Ser Ala Thr Cys Ala Gly Gly Lys Met Pro Thr Arg
 805 810 815
 Gln Pro Thr Gln Arg Ala Arg Trp Arg Thr Lys His Ile Leu Ser Tyr
 820 825 830
 Ala Leu Cys Leu Leu Lys Lys Leu Ile Gly Asn Ile Ser Cys Arg Phe
 835 840 845
 Ala Ser Ser Cys Asn Leu Ala Lys Glu Thr Leu Leu
 850 855 860

<210> 35
 <211> 936
 <212> PRT
 <213> Homo sapiens

<400> 35
 Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
 1 5 10 15
 Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
 20 25 30
 Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
 35 40 45
 Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
 50 55 60
 Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
 65 70 75 80
 Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu

85					90					95					
Asn	Asp	Gln	Asp	Asn	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile
			100					105					110		
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met
		115					120					125			
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys
	130					135					140				
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His
145					150					155					160
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly
				165					170					175	
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr
			180					185					190		
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val
		195					200					205			
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile
	210					215					220				
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu
225					230					235					240
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
				245					250					255	
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260					265					270		
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
		275					280					285			
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu
	290					295					300				
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp
305					310					315					320
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala
				325					330					335	
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val
			340					345					350		
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu
		355					360					365			
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro
	370					375					380				
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn

385		390		395		400
Val Val Glu Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile						
		405		410		415
Leu Gly Ser Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr						
		420		425		430
Gly Cys Gly Glu Gln Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val						
		435		440		445
Leu Asp Tyr Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser						
		450		455		460
Lys Ala Ile Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr						
		465		470		475
Lys His Tyr Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg						
		485		490		495
Asn Gln Gly Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala						
		500		505		510
Gln Ala Arg Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala						
		515		520		525
Leu Ile Trp Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser						
		530		535		540
Ser Gly Ser Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu						
		545		550		555
Val Thr Leu Ser Ala Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu						
		565		570		575
Thr Val Thr His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser						
		580		585		590
Ala Trp Lys Thr Ala Gln Glu Gly Asp His Gly Ser His Val Tyr Thr						
		595		600		605
Lys Ala Leu Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys						
		610		615		620
Arg Lys Glu Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp						
		625		630		635
Asn Ser Val His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly						
		645		650		655
His Phe Tyr Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser						
		660		665		670
Tyr Val Leu Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu						
		675		680		685
Asp Leu Thr Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln						

690					695					700					
Asn	Ala	Gln	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu
705					710					715					720
His	Ala	Leu	Ser	Lys	Tyr	Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys
				725					730					735	
Ala	Ala	Gln	Val	Thr	Ile	Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe
			740						745					750	
Gln	Val	Asp	Asn	Asn	Asn	Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro
		755					760					765			
Glu	Leu	Pro	Gly	Glu	Tyr	Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val
	770					775					780				
Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu
785					790					795					800
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu
			805						810					815	
Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr
			820					825					830		
Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val
		835					840					845			
Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser
	850					855					860				
Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr
865					870					875					880
Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu
			885					890						895	
Gln	Asp	Val	Pro	Val	Arg	Asp	Leu	Lys	Pro	Ala	Ile	Val	Lys	Val	Tyr
		900						905					910		
Asp	Tyr	Tyr	Glu	Thr	Gly	Glu	Phe	Ala	Ile	Ala	Glu	Tyr	Asn	Ala	Pro
	915						920					925			
Cys	Ser	Lys	Asp	Leu	Gly	Asn	Ala								
	930					935									

<210> 36
 <211> 898
 <212> PRT
 <213> Homo sapiens

<400> 36
 Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp
 1 5 10 15

Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
 20 25 30
 Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg
 35 40 45
 Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln
 50 55 60
 Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val
 65 70 75 80
 Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu
 85 90 95
 Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile
 100 105 110
 Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met
 115 120 125
 Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys
 130 135 140
 Ile Arg Lys Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro
 145 150 155 160
 Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala
 165 170 175
 Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly
 180 185 190
 Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala
 195 200 205
 Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr
 210 215 220
 Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn
 225 230 235 240
 Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro
 245 250 255
 Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile
 260 265 270
 Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser
 275 280 285
 Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln
 290 295 300
 Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys
 305 310 315 320

Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu Lys
 325 330 335
 Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val Ser
 340 345 350
 Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser Ala
 355 360 365
 Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met Gln
 370 375 380
 Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn
 385 390 395 400
 Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu
 405 410 415
 Thr Gln Gln Leu Thr Pro Glu Val Lys Ser Lys Ala Ile Gly Tyr Leu
 420 425 430
 Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser
 435 440 445
 Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp
 450 455 460
 Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile
 465 470 475 480
 Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln
 485 490 495
 Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn
 500 505 510
 Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr
 515 520 525
 Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val
 530 535 540
 Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln
 545 550 555 560
 Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr
 565 570 575
 Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys
 580 585 590
 Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu
 595 600 605
 Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln
 610 615 620

Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr
 625 630 635 640
 Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr
 645 650 655
 Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe
 660 665 670
 Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr
 675 680 685
 Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile
 690 695 700
 Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn
 705 710 715 720
 Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr
 725 730 735
 Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu
 740 745 750
 Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly
 755 760 765
 Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser
 770 775 780
 Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser
 785 790 795 800
 Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu
 805 810 815
 Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr
 820 825 830
 Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn
 835 840 845
 Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg
 850 855 860
 Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp
 865 870 875 880
 Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly
 885 890 895
 Asn Ala

<210> 37
 <211> 936

<212> PRT

<213> Homo sapiens

<400> 37

Arg	Leu	Leu	Ile	Tyr	Ala	Val	Leu	Pro	Thr	Gly	Asp	Val	Ile	Gly	Asp	
1				5					10					15		
Ser	Ala	Lys	Tyr	Asp	Val	Glu	Asn	Glu	Leu	Ala	Asn	Lys	Val	Asp	Leu	
			20					25					30			
Ser	Phe	Ser	Pro	Ser	Gln	Ser	Leu	Pro	Ala	Ser	His	Ala	His	Leu	Arg	
			35				40					45				
Val	Thr	Ala	Ala	Pro	Gln	Ser	Val	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln	
	50					55					60					
Ser	Val	Leu	Leu	Met	Lys	Pro	Asp	Ala	Glu	Leu	Ser	Ala	Ser	Ser	Val	
65					70					75					80	
Tyr	Asn	Leu	Leu	Pro	Glu	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Pro	Leu	
				85					90						95	
Asn	Asp	Gln	Asp	Asp	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile	
			100					105					110			
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met	
		115					120					125				
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys	
	130					135					140					
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His	
145					150					155					160	
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly	
				165					170					175		
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr	
			180					185						190		
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	
		195					200					205				
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	
		210				215					220					
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	
225					230					235					240	
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val	
				245					250					255		
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	
			260					265					270			
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val	
		275					280					285				

Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu	290	295	300	
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp	305	310	315	320
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	325	330	335	
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val	340	345	350	
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	355	360	365	
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	370	375	380	
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	385	390	395	400
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	405	410	415	
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	420	425	430	
Gly	Cys	Gly	Glu	Glx	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	435	440	445	
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser	450	455	460	
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	465	470	475	480
Lys	His	Tyr	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg	485	490	495	
Asn	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala	500	505	510	
Gln	Ala	Arg	Ala	Tyr	Ile	Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala	515	520	525	
Leu	Ile	Trp	Leu	Ser	Gln	Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	530	535	540	
Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu	545	550	555	560
Val	Thr	Leu	Ser	Ala	Tyr	Ile	Lys	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu	565	570	575	
Thr	Val	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser	580	585	590	

Ala	Trp	Lys	Thr	Ala	Glu	Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr	595	600	605
Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys	610	615	620
Arg	Lys	Glu	Val	Leu	Lys	Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp	625	630	635
Asn	Ser	Val	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly	645	650	655
His	Phe	Tyr	Glu	Pro	Gln	Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser	660	665	670
Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu	675	680	685
Asp	Leu	Thr	Ser	Ala	Thr	Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln	690	695	700
Asn	Ala	Gln	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Lys	Val	Val	Ala	Leu	705	710	715
His	Ala	Leu	Ser	Lys	Tyr	Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys	725	730	735
Ala	Ala	Gln	Val	Thr	Ile	Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe	740	745	750
Gln	Val	Asp	Asn	Asn	Asn	Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro	755	760	765
Glu	Leu	Pro	Gly	Glu	Tyr	Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	770	775	780
Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu	785	790	795
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu	805	810	815
Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr	820	825	830
Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val	835	840	845
Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	850	855	860
Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr	865	870	875
Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu	885	890	895

Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr
900 905 910

Asp Tyr Tyr Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro
915 920 925

Cys Ser Lys Asp Leu Gly Asn Ala
930 935

<210> 38
<211> 931
<212> PRT
<213> Rattus norvegicus

<400> 38
Arg Leu Val Leu Tyr Ala Ile Leu Pro Asn Gly Glu Val Val Gly Asp
1 5 10 15

Thr Ala Lys Tyr Glu Ile Glu Asn Cys Leu Ala Asn Lys Val Asp Leu
20 25 30

Val Phe Arg Pro Asn Ser Gly Leu Pro Ala Thr Arg Ala Leu Leu Ser
35 40 45

Val Met Ala Ser Pro Gln Ser Leu Cys Gly Leu Arg Ala Val Asp Gln
50 55 60

Ser Val Leu Leu Met Lys Pro Glu Thr Glu Leu Ser Ala Ser Leu Ile
65 70 75 80

Tyr Asp Leu Leu Pro Val Lys Asp Leu Thr Gly Phe Pro Gln Gly Ala
85 90 95

Asp Gln Arg Glu Glu Asp Thr Asn Gly Cys Val Lys Gln Asn Asp Thr
100 105 110

Tyr Ile Asn Gly Ile Leu Tyr Ser Pro Val Gln Asn Thr Asn Glu Glu
115 120 125

Asp Met Tyr Gly Phe Leu Lys Asp Met Gly Leu Lys Val Phe Thr Asn
130 135 140

Ser Asn Ile Arg Lys Pro Lys Val Cys Glu Arg Leu Arg Asp Asn Lys
145 150 155 160

Gly Ile Pro Ala Ala Tyr His Leu Val Ser Gln Ser His Met Asp Ala
165 170 175

Phe Leu Glu Ser Ser Glu Ser Pro Thr Glu Thr Arg Arg Ser Tyr Phe
180 185 190

Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val Asp Ser Ala Gly Val
195 200 205

Ala Glu Val Glu Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala

210					215					220					
Gly	Ala	Phe	Cys	Leu	Ser	Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Val
225					230					235					240
Val	Gln	Phe	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro
				245					250					255	
Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu
			260					265					270		
Asn	Tyr	Leu	Pro	Thr	Cys	Ile	Arg	Val	Ala	Val	Gln	Leu	Glu	Ala	Ser
		275					280					285			
Pro	Asp	Phe	Leu	Ala	Ala	Pro	Glu	Glu	Lys	Glu	Gln	Arg	Ser	His	Cys
	290					295					300				
Ile	Cys	Met	Asn	Gln	Arg	His	Thr	Ala	Ser	Trp	Ala	Val	Ile	Pro	Lys
305					310					315					320
Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Asn	Ser
			325						330					335	
Lys	Glu	Leu	Cys	Gly	Asn	Glu	Val	Pro	Val	Val	Pro	Glu	Gln	Gly	Lys
			340					345					350		
Lys	Asp	Thr	Ile	Ile	Lys	Ser	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu
	355						360					365			
Asn	Glu	Val	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Met	Gly	Ala	Glu	Val
	370					375					380				
Ser	Glu	Leu	Ile	Ala	Leu	Lys	Leu	Pro	Ser	Asp	Val	Val	Glu	Glu	Ser
385					390					395					400
Ala	Arg	Ala	Ser	Val	Thr	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met
			405						410					415	
Gln	Asn	Thr	Gln	Asp	Leu	Leu	Lys	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln
			420					425					430		
Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn
	435						440					445			
Glu	Thr	Gln	Gln	Leu	Thr	Gln	Glu	Ile	Lys	Thr	Lys	Ala	Ile	Ala	Tyr
	450					455					460				
Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly
465					470					475					480
Ser	Tyr	Ser	Ala	Phe	Gly	Asp	Lys	Pro	Gly	Arg	Asn	His	Ala	Asn	Thr
			485						490					495	
Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Lys	Tyr
			500					505					510		
Ile	Phe	Ile	Asp	Glu	Val	His	Ile	Thr	Gln	Ala	Leu	Leu	Trp	Leu	Ser

515					520					525						
Gln	Gln	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu	
530					535					540						
Asn	Asn	Ala	Met	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala	
545					550					555					560	
Tyr	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Met	Ser	Leu	Pro	Val	Thr	His	Pro	
565					570					575						
Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala	
580					585					590						
Arg	Gly	Gly	Ala	Gly	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	
595					600					605						
Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	
610					615					620						
Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala	Arg	Gly	Gly	Ala	Gly	Gly	Ser	His	
625					630					635					640	
Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro	
645					650					655						
Gln	Ala	Thr	Ser	Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Val	Leu	Leu	Ala	
660					665					670						
Tyr	Leu	Thr	Thr	Glu	Pro	Ala	Pro	Thr	Gln	Glu	Asp	Leu	Thr	Ala	Ala	
675					680					685						
Met	Leu	Ile	Val	Lys	Trp	Leu	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly	
690					695					700						
Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	
705					710					715					720	
Tyr	Gly	Ser	Ala	Thr	Phe	Thr	Arg	Ala	Lys	Lys	Ala	Ala	Gln	Val	Thr	
725					730					735						
Ile	Arg	Ser	Ser	Gly	Thr	Phe	Ser	Thr	Lys	Phe	Gln	Val	Asn	Asn	Asn	
740					745					750						
Asn	Gln	Leu	Leu	Leu	Gln	Arg	Val	Thr	Leu	Pro	Thr	Val	Pro	Gly	Asp	
755					760					765						
Tyr	Thr	Val	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser	
770					775					780						
Leu	Lys	Tyr	Ser	Val	Leu	Pro	Arg	Glu	Glu	Glu	Phe	Pro	Phe	Ala	Val	
785					790					795					800	
Val	Val	Gln	Thr	Leu	Pro	Gly	Thr	Cys	Glu	Asp	Pro	Lys	Ala	His	Thr	
805					810					815						
Ser	Phe	Gln	Ile	Ser	Leu	Asn	Ile	Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Glu	

820					825					830						
Ser	Asn	Met	Ala	Ile	Ala	Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro	
835					840					845						
Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	Val	His	Val	Ser	Arg	
850					855					860						
Thr	Glu	Val	Ser	Asn	Asn	His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	
865					870					875					880	
Asn	Gln	Thr	Val	Asn	Leu	Ser	Phe	Thr	Val	Gln	Gln	Asp	Ile	Pro	Ile	
885					890					895						
Arg	Asp	Leu	Lys	Pro	Ala	Val	Val	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Lys	
900					905					910						
Asp	Glu	Phe	Ala	Val	Ala	Lys	Tyr	Ser	Ala	Pro	Cys	Ser	Thr	Asp	Tyr	
915					920					925						
Gly	Asn	Ala														
930																

<210> 39
 <211> 941
 <212> PRT
 <213> Cavia porcellus

<400> 39

Arg	Val	Leu	Ile	Tyr	Ala	Ile	Leu	Pro	Ser	Gly	Glu	Ile	Ile	Ala	Asp
1				5					10					15	
Ser	Ala	Lys	Tyr	Asn	Val	Glu	Asn	Cys	Leu	Asp	Asn	Lys	Val	Asn	Leu
			20					25					30		
Ser	Phe	Ser	Glu	Gly	Gln	Ser	Leu	Pro	Ala	Ser	Lys	Thr	His	Leu	Arg
		35					40					45			
Val	Thr	Ala	Ser	Pro	Gln	Ser	Leu	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln
	50					55					60				
Ser	Val	Leu	Leu	Arg	Lys	Pro	Glu	Ala	Val	Leu	Ser	Ala	Ser	Ser	Val
65					70					75					80
Tyr	Ala	Leu	Leu	Pro	Val	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Leu	Leu
				85					90					95	
Gly	Gln	Gln	Glu	Glu	Asn	Asp	Gly	Glu	Cys	Val	Ser	Leu	Tyr	Asn	Thr
			100					105					110		
Tyr	Ile	Asp	Gly	Ile	Leu	Tyr	Ser	Pro	Glu	Pro	Asn	Ile	Asn	Glu	Lys
		115					120					125			
Asp	Met	Tyr	Gly	Phe	Leu	Lys	Asp	Met	Gly	Leu	Lys	Val	Phe	Thr	Asn
	130					135					140				

Thr	Lys	Ile	Gln	Lys	Pro	Gln	Leu	Cys	Ala	His	Val	Gln	Lys	Phe	Glu	145	150	155	160
Val	Pro	Thr	Met	Ala	Tyr	Ser	Tyr	Ser	Glu	Ser	Ser	Ser	Phe	Arg	Ser	165	170	175	
Gly	Pro	Arg	Arg	Val	Pro	Ala	Val	Gly	Ile	Ala	Ala	Thr	Tyr	Ser	Glu	180	185	190	
Pro	Pro	Lys	Glu	Thr	Val	Arg	Thr	Tyr	Ser	Pro	Glu	Thr	Trp	Ile	Trp	195	200	205	
Asp	Leu	Lys	Val	Thr	Asp	Ser	Ser	Gly	Val	Ala	Glu	Val	Glu	Val	Thr	210	215	220	
Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	225	230	235	240
Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Thr	Ala	Ser	Leu	Arg	Ala	Phe	245	250	255	
Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	260	265	270	
Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Asp	Cys	275	280	285	
Ile	Arg	Ile	Ser	Val	His	Leu	Glu	Ala	Ser	Pro	Lys	Phe	Leu	Ala	Glu	290	295	300	
Pro	Lys	Ala	Lys	Glu	Gln	Glu	Ser	Tyr	Cys	Val	Cys	Gly	Asn	Glu	Arg	305	310	315	320
Gln	Thr	Val	Ser	Trp	Val	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	325	330	335	
Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Ser	Glu	Leu	Cys	Gly	Asn	340	345	350	
Glu	Lys	Thr	Val	Val	Pro	Thr	Tyr	Gly	Lys	Lys	Asp	Thr	Ile	Ile	Lys	355	360	365	
Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Ile	Glu	Lys	Glu	Glu	Thr	Trp	Thr	370	375	380	
Ser	Leu	Ile	Arg	Val	Ser	Asp	Thr	Thr	Val	Ser	Glu	Lys	Leu	His	Leu	385	390	395	400
Glu	Leu	Pro	Ser	Asn	Val	Ile	Gln	Asp	Ser	Ala	Arg	Ala	Thr	Val	Ser	405	410	415	
Ile	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	Asn	Ile	Gln	Asn	Leu	420	425	430	
Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala	435	440	445	

Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	450	455	460	
Pro	Asp	Ile	Lys	Ser	Lys	Ala	Ile	Ser	Tyr	Leu	Ser	Thr	Gly	Tyr	Gln	465	470	475	480
Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly	485	490	495	
Glu	Asn	Tyr	Arg	Gly	Gly	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val	500	505	510	
Leu	Lys	Thr	Phe	Ser	Gln	Ala	Arg	Lys	Tyr	Ile	Phe	Ile	Asp	Glu	Ala	515	520	525	
His	Ile	Thr	Gln	Ala	Leu	Ser	Trp	Leu	Ser	Gln	Lys	Gln	Lys	Asp	Asn	530	535	540	
Gly	Cys	Phe	Trp	Ser	Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly	545	550	555	560
Gly	Val	Glu	Asp	Glu	Ile	Ser	Leu	Ser	Ala	Tyr	Ile	Thr	Ile	Ala	Leu	565	570	575	
Leu	Glu	Met	Ser	Leu	Pro	Asp	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	580	585	590	
Phe	Cys	Leu	Glu	Ser	Ala	Trp	Lys	Ser	Ala	Lys	Glu	Gly	Thr	His	Gly	595	600	605	
Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	610	615	620	
Gly	Asn	Gln	Glu	Arg	Lys	Lys	Glu	Ile	Leu	Lys	Ser	Leu	Glu	Asp	Glu	625	630	635	640
Gly	Val	Lys	Glu	Asp	Asn	Ser	Leu	His	Trp	Ala	Arg	Pro	Gln	Lys	Pro	645	650	655	
Lys	Val	Ser	Glu	Gly	Phe	Leu	Phe	Lys	Ser	Gln	Ala	Pro	Ser	Ala	Glu	660	665	670	
Val	Glu	Met	Thr	Ser	Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Arg	Pro	675	680	685	
Ala	Pro	Thr	Pro	Glu	Asp	Leu	Thr	Ser	Ala	Thr	Asp	Ile	Val	Asn	Trp	690	695	700	
Val	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly	Tyr	Ser	Ser	Thr	Gln	Asp	705	710	715	720
Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	Tyr	Ala	Ala	Ala	Thr	Phe	725	730	735	
Thr	Arg	Thr	Glu	Lys	Ala	Ala	Gln	Val	Thr	Ile	Lys	Ser	Ser	Gly	Thr	740	745	750	

Phe Ser Thr Asn Phe Glu Val Asn His Asn Asn Arg Leu Leu Leu Gln
 755 760 765
 Gln Val Ser Leu Pro Thr Val Ser Asp Ser Tyr Thr Ile Thr Val Thr
 770 775 780
 Gly Glu Gly Asn Val Tyr Leu Gln Thr Ser Leu Lys Tyr Asn Val Pro
 785 790 795 800
 Ser Glu Lys Gly Thr Phe Pro Phe Ala Leu Glu Ala Glu Thr Val Pro
 805 810 815
 Gln Ala Cys Asp Gly Pro Lys Ala His Thr Ser Phe Gln Ile Ser Leu
 820 825 830
 Asn Val Ser Tyr Ile Gly Ser Arg Pro Val Ser Asn Met Ala Ile Val
 835 840 845
 Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu Lys Pro Thr Val Lys
 850 855 860
 Asn Leu Glu Lys Ser Glu His Ile Ser Arg Thr Glu Val Ser Asn Asn
 865 870 875 880
 His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn Gln Thr Leu Ser Leu
 885 890 895
 Ser Phe Phe Val Val Gln Asp Ile Glu Val Arg Asp Leu Lys Pro Ala
 900 905 910
 Ile Ile Lys Val Tyr Asp Tyr Tyr Glu Thr Asn Glu Phe Ala Ile Ala
 915 920 925
 Glu Tyr His Ala Pro Cys Ser Lys Asp Pro Gly Asn Ala
 930 935 940

<210> 40
 <211> 373
 <212> PRT
 <213> Mus musculus

<400> 40
 Met Ser Thr Asp Cys Ala Gly Asn Ser Thr Cys Pro Val Asn Ser Thr
 1 5 10 15
 Glu Glu Asp Pro Pro Val Gly Met Glu Gly His Ala Asn Leu Lys Leu
 20 25 30
 Leu Phe Thr Val Leu Ser Ala Val Met Val Gly Leu Val Met Phe Ser
 35 40 45
 Phe Gly Cys Ser Val Glu Ser Gln Lys Leu Trp Leu His Leu Arg Arg
 50 55 60
 Pro Trp Gly Ile Ala Val Gly Leu Leu Ser Gln Phe Gly Leu Met Pro
 65 70 75 80

Leu Thr Ala Tyr Leu Leu Ala Ile Gly Phe Gly Leu Lys Pro Phe Gln
 85 90 95
 Ala Ile Ala Val Leu Met Met Gly Ser Cys Pro Gly Gly Thr Ile Ser
 100 105 110
 Asn Val Leu Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
 115 120 125
 Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
 130 135 140
 Leu Tyr Ile Tyr Thr Arg Ser Trp Thr Leu Thr Gln Asn Leu Val Ile
 145 150 155 160
 Pro Tyr Gln Ser Ile Gly Ile Thr Leu Val Ser Leu Val Val Pro Val
 165 170 175
 Ala Ser Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ala Thr Val
 180 185 190
 Ile Leu Lys Val Gly Ala Ile Leu Gly Gly Met Leu Leu Leu Val Val
 195 200 205
 Ala Val Thr Gly Met Val Leu Ala Lys Gly Trp Asn Thr Asp Val Thr
 210 215 220
 Leu Leu Val Ile Ser Cys Ile Phe Pro Leu Val Gly His Val Thr Gly
 225 230 235 240
 Phe Leu Leu Ala Phe Leu Thr His Gln Ser Trp Gln Arg Cys Arg Thr
 245 250 255
 Ile Ser Ile Glu Thr Gly Ala Gln Asn Ile Gln Leu Cys Ile Ala Met
 260 265 270
 Leu Gln Leu Ser Phe Ser Ala Glu Tyr Leu Val Gln Leu Leu Asn Phe
 275 280 285
 Ala Leu Ala Tyr Gly Leu Phe Gln Val Leu His Gly Leu Leu Ile Val
 290 295 300
 Ala Ala Tyr Gln Ala Tyr Lys Arg Arg Gln Lys Ser Lys Cys Arg Arg
 305 310 315 320
 Gln His Pro Asp Cys Pro Asp Val Cys Tyr Glu Lys Gln Pro Arg Glu
 325 330 335
 Thr Ser Ala Phe Leu Asp Lys Gly Asp Glu Ala Ala Val Thr Leu Gly
 340 345 350
 Pro Val Gln Pro Glu Gln His His Arg Ala Ala Glu Leu Thr Ser His
 355 360 365
 Ile Pro Ser Cys Glu
 370

260	265	270
Thr Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Thr Tyr Val Phe		
275	280	285
Thr Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile		
290	295	300
Phe Leu Gly Ile Tyr Val Ala Tyr Arg Lys Cys His Gly Lys Asn Asp		
305	310	315
Ala Glu Phe Pro Asp Ile Lys Asp Thr Lys Thr Glu Pro Glu Ser Ser		
325	330	335
Phe His Gln Met Asn Gly Gly Phe Gln Pro Glu		
340	345	

<210> 42
 <211> 348
 <212> PRT
 <213> Rattus norvegicus

<400> 42
Met Asp Asn Ser Ser Val Cys Ser Pro Asn Ala Thr Phe Cys Glu Gly
1 5 10 15
Asp Ser Cys Leu Val Thr Glu Ser Asn Phe Asn Ala Ile Leu Ser Thr
20 25 30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
35 40 45
Met Gly Cys Asn Val Glu Ile Asn Lys Phe Leu Gly His Ile Lys Arg
50 55 60
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
65 70 75 80
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
85 90 95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
100 105 110
Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
115 120 125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
130 135 140
Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
145 150 155 160
Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
165 170 175

Ser Ile Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190
 Ile Leu Lys Ile Gly Ser Ile Ala Gly Ala Ile Leu Ile Val Leu Ile
 195 200 205
 Ala Val Val Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
 210 215 220
 Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
 225 230 235 240
 Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255
 Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285
 Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Ile Ile
 290 295 300
 Leu Gly Met Tyr Val Thr Tyr Lys Lys Cys His Gly Lys Asn Asp Ala
 305 310 315 320
 Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe
 325 330 335
 Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345

<210> 43
 <211> 348
 <212> PRT
 <213> Mus musculus

<400> 43
 Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly
 1 5 10 15
 Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr
 20 25 30
 Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser
 35 40 45
 Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg
 50 55 60
 Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro
 65 70 75 80
 Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln
 85 90 95

Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser
 100 105 110
 Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser
 115 120 125
 Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys
 130 135 140
 Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile
 145 150 155 160
 Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val
 165 170 175
 Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile
 180 185 190
 Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile
 195 200 205
 Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro
 210 215 220
 Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu
 225 230 235 240
 Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255
 Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285
 Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile
 290 295 300
 Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala
 305 310 315 320
 Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe
 325 330 335
 Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345

<210> 44

<211> 348

<212> PRT

<213> Mus musculus

<400> 44

Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly

1	5	10	15
Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr	20	25	30
Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser	35	40	45
Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg	50	55	60
Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro	65	70	75
Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln	85	90	95
Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser	100	105	110
Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser	115	120	125
Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys	130	135	140
Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile	145	150	155
Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val	165	170	175
Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile	180	185	190
Ile Leu Lys Ile Gly Ser Ile Thr Gly Val Ile Leu Ile Val Leu Ile	195	200	205
Ala Val Ile Gly Gly Ile Leu Tyr Gln Ser Ala Trp Ile Ile Glu Pro	210	215	220
Lys Leu Trp Ile Ile Gly Thr Ile Phe Pro Ile Ala Gly Tyr Ser Leu	225	230	235
Gly Phe Phe Leu Ala Arg Leu Ala Gly Gln Pro Trp Tyr Arg Cys Arg	245	250	255
Thr Val Ala Leu Glu Thr Gly Met Gln Asn Thr Gln Leu Cys Ser Thr	260	265	270
Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr	275	280	285
Phe Pro Leu Ile Tyr Thr Val Phe Gln Leu Val Phe Ala Ala Val Ile	290	295	300
Leu Gly Ile Tyr Val Thr Tyr Arg Lys Cys Tyr Gly Lys Asn Asp Ala			

Lys Leu Trp Ile Ile Gly Thr Ile Tyr Pro Ile Ala Gly Tyr Gly Leu
 225 230 235 240
 Gly Phe Phe Leu Ala Arg Ile Ala Gly Gln Pro Trp Tyr Arg Cys Arg
 245 250 255
 Thr Val Ala Leu Glu Thr Gly Leu Gln Asn Thr Gln Leu Cys Ser Thr
 260 265 270
 Ile Val Gln Leu Ser Phe Ser Pro Glu Asp Leu Asn Leu Val Phe Thr
 275 280 285
 Phe Pro Leu Ile Tyr Ser Ile Phe Gln Ile Ala Phe Ala Ala Ile Leu
 290 295 300
 Leu Gly Ala Tyr Val Ala Tyr Lys Lys Cys His Gly Lys Asn Asn Thr
 305 310 315 320
 Glu Leu Gln Glu Lys Thr Asp Asn Glu Met Glu Pro Arg Ser Ser Phe
 325 330 335
 Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys
 340 345

<210> 46
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 46
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Phe Thr Ser Ile Gly Glu
 100 105 110
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys
 115 120 125
 Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu
 130 135 140

Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr
 145 150 155 160
 Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly
 165 170 175
 Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu
 180 185 190
 Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys
 195 200 205
 Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile
 210 215 220
 Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys
 225 230 235 240
 Leu Glu Ala Ala Glu Asp Ile Ala Tyr Gln Leu Ser Arg Ser Arg Asn
 245 250 255
 Ile Thr Tyr Leu Pro Ala Gly Gln Ser Val Leu Leu Gln Leu Pro Gln
 260 265 270

<210> 47
 <211> 272
 <212> PRT
 <213> Rattus norvegicus

<400> 47
 Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu
 1 5 10 15
 Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala
 20 25 30
 Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile
 35 40 45
 Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro
 50 55 60
 Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr
 65 70 75 80
 Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe
 85 90 95
 Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Tyr Thr Ser Ile Gly Glu
 100 105 110
 Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys

115					120					125						
Ser	Val	Val	Ala	Arg	Phe	Asp	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Arg	Glu	
130					135					140						
Leu	Val	Ser	Arg	Gln	Val	Ser	Asp	Asp	Leu	Thr	Glu	Arg	Ala	Ala	Thr	
145					150					155					160	
Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	His	Leu	Thr	Phe	Gly	
165					170					175						
Lys	Glu	Phe	Thr	Glu	Ala	Val	Glu	Ala	Lys	Gln	Val	Ala	Gln	Gln	Glu	
180					185					190						
Ala	Glu	Arg	Ala	Arg	Phe	Val	Val	Glu	Lys	Ala	Glu	Gln	Gln	Lys	Lys	
195					200					205						
Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Ala	Ala	Glu	Leu	Ile	
210					215					220						
Ala	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu	Arg	Lys	
225					230					235					240	
Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ala	Tyr	Gln	Leu	Ser	Arg	Ser	Arg	Asn	
245					250					255						
Ile	Thr	Tyr	Leu	Pro	Ala	Gly	Gln	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln	
260					265					270						

<210> 48
 <211> 1798
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 48															
Met	Glu	Met	Arg	Glu	Val	Leu	Ser	Arg	Glu	Gly	Arg	Glu	Ala	Lys	Asn
1				5					10					15	
Leu	Leu	Val	Tyr	Gln	Phe	Cys	Asp	Glu	Thr	Thr	Ser	Ser	Gly	Ala	Thr
20				25				30							
Ser	Gly	Phe	Gly	Ser	Thr	Gly	Gly	Asp	Val	Gly	Gly	Gly	Ser	Gly	Gly
35				40				45							
Asp	Gly	Pro	Ala	Val	Gly	Ser	Gly	Gly	Val	Leu	Leu	Asn	Gly	Asp	Cys
50				55				60							
Tyr	Arg	Lys	Pro	Pro	Met	Val	Pro	Pro	Lys	Ser	Pro	Asn	Gly	Thr	Pro
65				70				75				80			
Lys	Asn	Cys	Gln	Ser	Pro	Thr	Ser	Pro	Arg	Leu	Lys	Ser	Ser	Ala	Ser
85					90					95					

Val	Gly	Cys	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Pro	Arg	Val	Arg	Ser	Ala		
			100					105					110				
Ser	Thr	Gly	Arg	Asp	Lys	Lys	Ser	Glu	Leu	Gln	Ala	Arg	Tyr	Trp	Ala		
		115					120					125					
Leu	Leu	Phe	Gly	Asn	Leu	Gln	Arg	Ala	Ile	Asn	Glu	Ile	Tyr	Gln	Thr		
		130				135					140						
Val	Glu	Cys	Tyr	Glu	Asn	Ile	Ser	Ser	Cys	Gln	Glu	Thr	Ile	Leu	Val		
145					150					155					160		
Leu	Glu	Asn	Tyr	Val	Arg	Asp	Phe	Lys	Ala	Leu	Cys	Glu	Trp	Phe	Lys		
				165				170						175			
Val	Ser	Trp	Asp	Tyr	Glu	Ser	Arg	Pro	Leu	Gln	Gln	Arg	Pro	Gln	Ser		
			180					185					190				
Leu	Ala	Trp	Glu	Val	Arg	Lys	Ser	Asn	Pro	Thr	Pro	Arg	Val	Arg	Thr		
		195					200					205					
Arg	Ser	Leu	Cys	Ser	Pro	Asn	Asn	Ser	Gly	Lys	Ser	Ser	Pro	Ala	Leu		
		210				215					220						
Phe	Pro	Gly	Thr	Gln	Ser	Gly	Glu	Thr	Ser	Pro	Phe	Cys	Asp	Asn	Gly		
225					230					235					240		
Gln	Ile	Ser	Pro	Arg	Lys	Leu	Leu	Arg	Ala	Tyr	Asp	Gln	Val	Pro	Lys		
				245					250					255			
Gly	Ala	Met	Arg	Leu	Asn	Val	Arg	Glu	Leu	Phe	Ala	Ala	Ser	Lys	Arg		
			260					265					270				
Ala	Thr	Gln	Gly	Ser	Ser	Gln	Ser	Asp	Asn	Met	Glu	Gly	Pro	Leu	Asp		
		275					280					285					
Leu	Ser	Gly	Asp	Lys	Ser	Asn	Phe	Val	Leu	Arg	Ser	Thr	Gln	Tyr	Ala		
		290				295					300						
Gln	Thr	Asp	Leu	Glu	Asp	Pro	His	Leu	Thr	Leu	Ala	Asp	Val	Arg	Glu		
305					310					315					320		
Lys	Met	Arg	Met	Glu	Ala	Glu	Glu	Arg	Glu	Ala	Gln	Asn	Arg	Ile	Glu		
				325					330					335			
Asn	Glu	Ala	Leu	Glu	Glu	Val	Thr	Ile	Pro	Ile	Asp	Asn	Glu	Asp	Ala		
			340					345					350				
Thr	Glu	Ser	Leu	Asn	Lys	Gln	Glu	Pro	Ser	Ser	Leu	Glu	Leu	Pro	Ile		
		355					360					365					
His	Asn	Val	Ala	Asp	Leu	Ser	Lys	Glu	Pro	Glu	Leu	Met	Glu	Ala	Ala		
		370				375					380						
Ser	Glu	Ala	Thr	Ala	Leu	Glu	Met	Thr	Val	Ala	Ser	Leu	Glu	Ser	Met		
385					390					395					400		

Glu Asn Ala Leu Leu Asn Gln Gln Ala Asn Lys Glu Pro Thr Pro Pro
 405 410 415
 Ser Thr Val Ile Lys Pro Leu Ala Glu Ile Leu Lys Lys Pro Gln Pro
 420 425 430
 Leu Asn Pro Leu Ser Gly Asn Asn Val Gln Asn Ser Pro Leu Lys Tyr
 435 440 445
 Ser Ser Val Leu Asn Arg Pro Ser Lys Lys Met Ile Pro Pro Pro Gly
 450 455 460
 Gly Val Ala Ala Gln Lys Thr Ile Ser Thr Lys Pro Gly Leu Val Lys
 465 470 475 480
 Pro Asn Leu Thr Thr Thr Val Asn Gly Leu Arg Ser Thr Lys Thr Ala
 485 490 495
 Thr Ala Pro Pro Ala Ile Lys Thr Thr Gly Arg Ser Gly Leu Gln Arg
 500 505 510
 His Pro Arg Pro Ser Ser Lys Thr Glu Cys Tyr Gly Pro Pro Asn Asn
 515 520 525
 Val Ala Ser Arg Leu Ser Ala Arg Ser Arg Thr Ile Asn Thr Leu Lys
 530 535 540
 Ala Glu Asn Gln His Ser Glu Pro Lys Gln Ile Gln Pro Pro Thr Asp
 545 550 555 560
 Ala Asp Asp Gly Trp Leu Thr Val Lys Asn Arg Arg Arg Thr Ser Met
 565 570 575
 His Trp Ala Asn Arg Phe Asn Gln Pro Thr Gly Tyr Ala Ser Leu Pro
 580 585 590
 Thr Leu Ala Leu Leu Asn Glu Gln Gln Lys Glu Gln Glu His Lys Glu
 595 600 605
 Lys Gln Lys Gly Glu Asp Asp Gly Lys Val Ile Val Lys Thr Ile Ser
 610 615 620
 Ala Lys Thr Lys Ala Pro Ile Glu Val Ala Lys Ala Lys Ala Lys Thr
 625 630 635 640
 Ser Ile Val Ile Thr Arg Pro Glu Ile Lys Asn Ala Lys Ala Lys Val
 645 650 655
 Asn Ser Phe Pro Val Gln Lys Ser Asn Thr Asn Gln Val Lys Lys Pro
 660 665 670
 Glu Lys Gln Glu Lys Ser Asp Thr Thr Ala Pro Ala Ala Ile Ala Ser
 675 680 685
 Ser Arg Leu Lys Met Thr Ser Leu His Lys Glu Tyr Met Arg Ser Glu
 690 695 700

Lys Asn Ala Leu Arg Lys Leu Gln Gln Lys Glu Gln Gly Asn Gln Gln
 705 710 715 720
 His Asn Ser Ser Ser Ser Ser Ala Glu Thr Val Val Glu Ser Cys Asn
 725 730 735
 Glu Asp His Ser Lys Ile Asp Ile Lys Ile Gln Thr Asn Cys Glu Phe
 740 745 750
 Ser Lys Thr Ile Gly Glu Leu Tyr Glu Ser Ile Ala His Cys Lys Leu
 755 760 765
 Pro Ser Gly Ser Leu Lys Thr Asn Ala Ser Thr Leu Ser Ala Cys Asp
 770 775 780
 Glu Asn Glu Glu Gln Asn Thr Asp Asp Asn Glu Glu Glu Arg Asn Glu
 785 790 795 800
 Arg Ile Leu Gly Glu Val Gln Glu Ser Leu Glu Arg Gln Ile Arg Glu
 805 810 815
 Leu Glu Gln Thr Glu Ile Asp Val Asp Thr Glu Thr Asp Glu Thr Asp
 820 825 830
 Cys Glu Val Gln Leu Glu Glu Gln Asp Asp Gly Val Asp Gly Leu Glu
 835 840 845
 Met Gly Ser Gly Asp Asp Ser Ala Val Phe Val Thr Met Ser Asp Asp
 850 855 860
 Glu Asn Ala Ser Leu Glu Leu Arg Tyr Gln Ala Leu Leu Ser Asp Met
 865 870 875 880
 Ser Trp Asn Glu Arg Ala Glu Ala Leu Ala Thr Leu Gln Ala Tyr Val
 885 890 895
 Ala Arg His Pro Gly Arg Ala Gln Glu Leu His Gln Lys Leu Ser Ser
 900 905 910
 Pro Ser Arg Arg Arg Ser Leu Gln Glu Thr Leu Lys Lys Tyr Gln Ala
 915 920 925
 Lys Gln Ala Arg Ala Gln Gln Lys Arg Asn Leu Leu Gln Gln Glu Lys
 930 935 940
 Ala Ala Lys Leu Gln Gln Leu Phe Ser Arg Val Glu Asp Val Lys Ala
 945 950 955 960
 Ala Lys Asn Gln Ile Ile Glu Asp Lys Arg Gln Lys Met Gln Gly Arg
 965 970 975
 Leu Gln Arg Ala Ala Glu Asn Arg Glu Gln Tyr Leu Lys Gln Ile Ile
 980 985 990
 Glu Lys Ala His Asp Glu Glu Lys Lys Leu Lys Glu Ile Asn Phe Ile
 995 1000 1005

Lys Asn Ile Glu Ala Gln Asn Lys Arg Leu Asp Leu Leu Glu Ser Ser
 1010 1015 1020
 Lys Glu Thr Glu Gly Arg Leu Gln Asp Leu Glu Gln Glu Arg Gln Lys
 1025 1030 1035 1040
 Arg Val Glu Glu Lys Leu Ala Lys Glu Ala Ala Val Glu Arg Arg Arg
 1045 1050 1055
 Gln Ala Leu Glu Lys Glu Arg Leu Leu Lys Leu Glu Lys Met Asn Glu
 1060 1065 1070
 Thr Arg Leu Glu Lys Glu Gln Arg Ile Gly Lys Met Gln Glu Gln Lys
 1075 1080 1085
 Glu Lys Gln Arg Gln Ala Leu Ala Arg Glu Lys Ala Arg Asp Arg Glu
 1090 1095 1100
 Glu Arg Leu Leu Ala Leu Gln Val Gln Gln Gln Gln Thr Thr Glu Glu
 1105 1110 1115 1120
 Leu Gln Arg Lys Ile Leu Gln Lys Gln Met Glu Ser Ala Arg Arg His
 1125 1130 1135
 Glu Glu Asn Ile Glu His Ile Arg Gln Arg Ala Leu Glu Leu Thr Ile
 1140 1145 1150
 Pro Thr Arg Gln Ala Asp Glu Gly Arg Gly Asp Gln Asp Val Ser Glu
 1155 1160 1165
 Asp Ile Leu Asn Gly Asn Ala Thr Ser Thr Thr Asn Glu Asp Cys Asp
 1170 1175 1180
 Leu Ser Ser Ser Leu Ser Glu Val Gly Gly Asn Asn Ala His Thr Arg
 1185 1190 1195 1200
 Ser Tyr Lys Lys Lys Met Lys Lys Leu Lys Gln Arg Met Asn Gln Cys
 1205 1210 1215
 Ala Ala Glu Tyr Leu Glu Ser Leu Glu Ala Leu Pro Ala His Ala Arg
 1220 1225 1230
 Arg Asp Ser Thr Val Pro Lys Leu Leu Asn Leu Val Val Lys Gly Gly
 1235 1240 1245
 Gly Ala Gln Gly Leu Asp Arg Asn Leu Gly Asn Leu Leu Arg Val Ile
 1250 1255 1260
 Pro Lys Ala Gln Thr Leu Asp Phe Leu Ala Phe Leu Cys Met Asp Gly
 1265 1270 1275 1280
 Leu Gly Ile Leu Ala Asn His Val Ile Ser Lys Gly Met Asp Glu Asn
 1285 1290 1295
 Ser Glu Ile Ser Arg Lys Ser Val Tyr Leu Ala Ala Gln Leu Tyr Arg
 1300 1305 1310

Asn Ala Cys Ser Val Cys Pro Gln Ile Ala Arg His Ala Leu Leu Gly
 1315 1320 1325
 Asn Ser Ile Thr Val Leu Phe Asp Ala Ile Asn Lys Ser Phe Gln Val
 1330 1335 1340
 Ile Leu Lys Ser Asn Arg Cys Thr Lys Glu Thr Phe Ser Asn Phe Trp
 1345 1350 1355 1360
 Pro Pro Lys Met Leu His Asn Lys Ser Val Ala Arg Gln Ser Ser Arg
 1365 1370 1375
 Leu Glu Ala Leu Ser Leu Pro Glu Glu Lys Ser Pro Gln His Pro Val
 1380 1385 1390
 Glu Leu Ser Thr Glu Leu Met Leu Ala Cys Thr Glu Ala Leu Ser Ser
 1395 1400 1405
 Ser Tyr Val Lys Lys Asn Thr His Pro Lys Val Pro Glu Arg Leu Pro
 1410 1415 1420
 Asp Met Ile Asn Asp Cys Arg Phe His Trp Gln Asp Val Asn Lys Glu
 1425 1430 1435 1440
 Asp Met Leu Ala Asp Glu Phe Arg Lys Tyr Lys Cys Tyr Glu Lys Asn
 1445 1450 1455
 Pro Val Ile Ala Leu Pro His Pro Ser Leu Ser Ala Ser Leu Cys Arg
 1460 1465 1470
 Ser Leu Ser Ala Thr Pro Leu Lys Ile Asn Leu His Gln Phe Leu Gly
 1475 1480 1485
 Ser Gly Ile Leu Ile Leu Arg Leu Asn His His Arg His Pro Ala Thr
 1490 1495 1500
 Gly Ala Ser Phe Ser Asp Ser Cys Cys Thr Cys Cys Pro Lys Leu Thr
 1505 1510 1515 1520
 Thr Glu Ala Ala Val Ala Ala Val Ala Ala His Gln His Gln His Gln
 1525 1530 1535
 Asn Gln Gln Gln Gln Pro Asp Tyr Ala Val Ile Thr Gly Leu Ile Glu
 1540 1545 1550
 Ile Leu Ser Arg Arg Ile Gln Lys Val Arg Glu Ser Ile Glu Ser Asn
 1555 1560 1565
 Lys Ser Val Met Leu Ser Leu Leu Thr Thr Leu Gly Phe Leu Ser Arg
 1570 1575 1580
 Phe Ile Asp Val Cys Gln Pro Gly Pro Ala Asp Pro Thr Arg Leu Leu
 1585 1590 1595 1600
 Ser Ala Ala Lys Ser Thr Glu Leu Phe Gly Thr Val Ser Met Leu Tyr
 1605 1610 1615

Gly Cys Val Met Pro Met Gly Glu Cys Ile Pro Pro Arg Thr Thr Ala
 1620 1625 1630
 Leu Ala Ala Ser Thr Phe His Leu Tyr Val Ser Leu Ala Ser Leu Asp
 1635 1640 1645
 Val Asn Thr Phe Gln Glu Thr Leu Thr Val Glu Gly Pro Leu Ser Leu
 1650 1655 1660
 Lys Leu Leu Asp Val Met Thr Val Ile Leu Asn Cys Ser Leu Val Asn
 1665 1670 1675 1680
 Asp Gln Trp Thr Thr Asn Ser Glu Ser Cys Pro Met Leu Ile Asp Leu
 1685 1690 1695
 Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp
 1700 1705 1710
 Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys
 1715 1720 1725
 Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val
 1730 1735 1740
 Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp
 1745 1750 1755 1760
 Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn
 1765 1770 1775
 Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala
 1780 1785 1790
 Gly Asn Lys Lys Asn Ala
 1795

<210> 49
 <211> 274
 <212> PRT
 <213> *Toxocara canis*

<400> 49
 Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val
 1 5 10 15
 Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val
 20 25 30
 Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys
 35 40 45
 Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln
 50 55 60
 Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr
 65 70 75 80

Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Ser Ile Thr Leu Arg Ile
 85 90 95
 Leu His Arg Pro Glu Pro Ser Lys Leu Pro Asn Ile Tyr Leu Asn Ile
 100 105 110
 Gly Gln Asp Tyr Ala Glu Arg Val Leu Pro Ser Ile Thr Asn Glu Val
 115 120 125
 Leu Lys Ala Val Val Ala Gln Phe Asp Ala His Glu Met Ile Thr Gln
 130 135 140
 Arg Glu Ser Val Ser His Arg Val Ser Val Glu Leu Ser Glu Arg Ala
 145 150 155 160
 Arg Gln Phe Gly Ile Leu Leu Asp Asp Ile Ala Ile Thr His Leu Ser
 165 170 175
 Phe Gly Arg Glu Phe Thr Glu Ala Val Glu Met Lys Gln Val Ala Gln
 180 185 190
 Gln Glu Ala Glu Lys Ala Arg Tyr Leu Val Glu Thr Ala Glu Gln Met
 195 200 205
 Lys Ile Ala Ala Ile Thr Thr Ala Glu Gly Asp Ala Gln Ala Ala Lys
 210 215 220
 Leu Leu Ala Gln Ala Phe Lys Asp Ala Gly Asp Gly Leu Ile Glu Leu
 225 230 235 240
 Arg Lys Ile Glu Ala Ala Glu Glu Ile Ala Glu Arg Met Ser Lys Thr
 245 250 255
 Arg Asn Val Ile Tyr Leu Pro Gly Asn Gln Asn Thr Leu Phe Asn Leu
 260 265 270

Pro Ala

<210> 50

<211> 402

<212> PRT

<213> Caenorhabditis elegans

<400> 50

Met Glu Lys Tyr Lys Asn Glu Leu Glu Ile Phe Lys Arg Met Tyr Phe
 1 5 10 15

Lys Asn Tyr Pro Thr Ser Ser Lys Asp Glu Glu Ala Ala Ala Val Ile
 20 25 30

Gln Lys Gly Gly Glu Phe Ile Gln Glu Ile Leu Pro Thr Ile Ile Ser
 35 40 45

Thr Ser Arg Ala Tyr Asp Thr Asn Gln Lys Ala Leu Leu Leu Ala Glu

50	55	60
Gly Gly Lys Met Tyr Asn Val Leu Glu Asp Tyr Asn Glu Thr Ala Glu		
65	70	75 80
Lys Met Leu Ser Lys Ser Val Arg Met Asn Pro Lys Asn Ala Asp Ala		
	85	90 95
Trp His Glu Leu Gly Leu Cys Val Met Lys Arg Arg Asp Leu Glu Phe		
	100	105 110
Ala Gln Ser Cys Phe Lys Ile Ala Leu Gly Ile Ser Lys Thr Ala Pro		
	115	120 125
Ile Leu Thr Ser Leu Ala Val Ala Met Arg Leu Val Ala Leu Glu His		
	130	135 140
Pro Glu Pro Ala Gln Ala Glu Ile Arg Thr Lys Ala Met Glu Leu Ile		
	145	150 155 160
Ile Glu Ala Arg Arg Leu Asp Ser Ala Tyr Gly Pro Ala Asn Ile Ala		
	165	170 175
Phe Ala Thr Gly Leu Phe Tyr Cys Phe Phe Ser Thr Ala Lys Val Glu		
	180	185 190
Leu Lys Phe Leu Asp Lys Val Ile Glu Asn Tyr Lys Lys Ala Leu Glu		
	195	200 205
Cys Glu Leu Ser Arg Thr Asp Pro Gln Val Tyr Ile Asn Met Ala Thr		
	210	215 220
Cys Leu Lys Phe Met Glu Lys Tyr Asp Glu Ala Leu Ala Val Leu Gln		
	225	230 235 240
Lys Ala Val Glu Tyr Asp Pro Arg Asn Glu Leu Glu Thr Arg Glu Lys		
	245	250 255
Leu Ala Ser Phe Val Ser Tyr Leu Ser Lys Phe Thr Asp Ala Ile Gln		
	260	265 270
Lys Lys Gly Lys Met Lys Ala Lys Arg Met Gln Glu Met Ile Asn Glu		
	275	280 285
Leu Lys Lys Ser Ser Asp Gly Phe Arg Ala Lys Ile Ile Gly Asn Ile		
	290	295 300
Gly His Asp Glu Thr Ile Pro Val Ala Leu Val Gly Val Asp Ala Ala		
	305	310 315 320
Gly Glu Val Tyr Gly Ile Thr Ile Tyr Asn Cys Leu Ser Asn Phe Gly		
	325	330 335
Phe Val Ile Gly Asp Thr Val Thr Ile Ala Lys Pro Asp Phe Arg Glu		
	340	345 350
Ile Lys Asn Leu Thr Ile Pro Ser Asp Pro Glu Ile His Val Asp Ser		

355 360 365
 Val Lys Trp Ile Arg Val Ala Thr Pro Thr Gln Met Lys Lys Asn Gly
 370 375 380
 Val Pro Leu Pro Glu Ser Val Leu Ala Arg Ala Val Ala Ser Thr Gln
 385 390 395 400
 Thr Lys

 <210> 51
 <211> 711
 <212> PRT
 <213> Homo sapiens

 <400> 51
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
 1 5 10 15
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
 20 25 30
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
 85 90 95
 Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
 100 105 110
 Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
 115 120 125
 Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
 130 135 140
 Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
 145 150 155 160
 Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
 165 170 175
 Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
 180 185 190
 Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
 195 200 205

Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	210	215	220	
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	225	230	235	240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250	255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	260	265	270	
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	275	280	285	
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	290	295	300	
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	305	310	315	320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	325	330	335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	340	345	350	
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	355	360	365	
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys	370	375	380	
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	385	390	395	400
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	405	410	415	
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	420	425	430	
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	435	440	445	
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln	450	455	460	
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser	465	470	475	480
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val	485	490	495	
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val	500	505	510	

Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys His
 515 520 525
 Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln Asn
 530 535 540
 Pro Gln His Gly Glu Pro Ser Leu Gln Arg Val Pro Val Ala Lys Met
 545 550 555 560
 Val Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu Arg
 565 570 575
 Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro Glu
 580 585 590
 Trp Tyr Val Val Pro Pro Gly Thr Lys Cys Glu Ile Ala Gly Trp Gly
 595 600 605
 Glu Thr Lys Gly Thr Gly Asn Asp Thr Val Leu Asn Val Ala Leu Leu
 610 615 620
 Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val
 625 630 635 640
 Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala
 645 650 655
 Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys
 660 665 670
 Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
 675 680 685
 Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
 690 695 700
 His Lys Val Met Arg Leu Gly
 705 710

<210> 52
 <211> 711
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
 1 5 10 15
 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
 20 25 30
 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
 50 55 60

Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Val	Ser	Ser	His	Gly	Cys	Gln	Leu	65	70	75	80
Leu	Pro	Trp	Thr	Gln	His	Ser	Pro	His	Thr	Arg	Leu	Arg	Arg	Ser	Gly	85	90	95	
Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met	100	105	110	
Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly	115	120	125	
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr	130	135	140	
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro	145	150	155	160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val	165	170	175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val	180	185	190	
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser	195	200	205	
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro	210	215	220	
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys	225	230	235	240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	245	250	255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala	260	265	270	
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly	275	280	285	
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	290	295	300	
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu	305	310	315	320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	325	330	335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	340	345	350	
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	355	360	365	

Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys	
370						375					380					
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	
385					390					395					400	
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	
				405					410					415		
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	
			420					425					430			
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	
		435					440					445				
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln	
	450					455					460					
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser	
465					470					475					480	
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val	
				485					490					495		
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val	
			500					505					510			
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His	
		515					520					525				
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn	
	530					535					540					
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met	
545					550					555					560	
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg	
				565					570					575		
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu	
			580					585					590			
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly	
		595					600					605				
Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val	Leu	Asn	Val	Ala	Phe	Leu	
						615					620					
Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile	Lys	His	Arg	Gly	Arg	Val	
625					630					635					640	
Arg	Glu	Ser	Glu	Met	Cys	Thr	Glu	Gly	Leu	Leu	Ala	Pro	Val	Gly	Ala	
				645					650					655		
Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys	Phe	Thr	His	Asn	Cys	
			660					665					670			

Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser
675 680 685

Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile
690 695 700

His Lys Val Met Arg Leu Gly
705 710

<210> 53
<211> 711
<212> PRT
<213> Homo sapiens

<400> 53
Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
115 120 125

Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
130 135 140

Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
145 150 155 160

Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
165 170 175

Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val
180 185 190

Trp Cys Asn Gly Glu Glu Tyr Arg Gly Ala Val Asp Arg Thr Glu Ser
195 200 205

Gly Arg Glu Cys Gln Arg Trp Asp Leu Gln His Pro His Gln His Pro

210					215					220					
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala
			260					265					270		
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly
		275					280					285			
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys
	290					295					300				
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu
305					310					315					320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp
				325					330					335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala
			340					345					350		
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln
		355					360					365			
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys
	370					375					380				
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His
385					390					395					400
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu
			405						410				415		
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr
			420					425					430		
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys
		435					440					445			
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln
	450					455					460				
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser
465					470					475					480
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val
			485						490				495		
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val
			500				505						510		
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His

515					520					525					
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn
530					535					540					
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met
545					550					555					
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg
565					570					575					
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu
580					585					590					
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly
595					600					605					
Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val	Leu	Asn	Val	Ala	Leu	Leu
610					615					620					
Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile	Lys	His	Arg	Gly	Arg	Val
625					630					635					
Arg	Glu	Ser	Glu	Met	Cys	Thr	Glu	Gly	Leu	Leu	Ala	Pro	Val	Gly	Ala
645					650					655					
Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys	Phe	Thr	His	Asn	Cys
660					665					670					
Trp	Val	Leu	Glu	Gly	Ile	Ile	Ile	Pro	Asn	Arg	Val	Cys	Ala	Arg	Ser
675					680					685					
Arg	Trp	Pro	Ala	Val	Phe	Thr	Arg	Val	Ser	Val	Phe	Val	Asp	Trp	Ile
690					695					700					
His	Lys	Val	Met	Arg	Leu	Gly									
705					710										

<210> 54
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 54															
Met	Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Val	Ser	Ser	His	Gly	Cys	Gln
1				5					10					15	
Leu	Leu	Pro	Trp	Thr	Gln	His	Ser	Pro	His	Thr	Arg	Leu	Arg	His	Ser
			20					25				30			
Gly	Arg	Cys	Asp	Leu	Phe	Gln	Glu	Lys	Asp	Tyr	Ile	Arg	Thr	Cys	Ile
		35					40					45			
Met	Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly
	50					55				60					

Gly	Leu	Ser	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Gln	
65					70					75					80	
Tyr	Met	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	
				85					90					95		
Pro	Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	His	Thr	Thr	Asp	Pro	Ala	
			100					105					110			
Val	Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Val	Ala	Ala	Cys	
		115					120					125				
Val	Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	
	130					135					140					
Ser	Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	
145					150					155					160	
Pro	Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	
				165					170					175		
Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	
			180					185					190			
Pro	Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	
		195					200					205				
Ala	Gln	Pro	Arg	Gln	Glu	Ala	Thr	Ser	Val	Ser	Cys	Phe	Arg	Gly	Lys	
		210				215					220					
Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	
225					230					235					240	
Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	
				245					250					255		
Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	
			260					265					270			
Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	
		275					280					285				
Val	Gly	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	
	290					295					300					
Gln	Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	
305					310					315					320	
Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Gly	Ser	Ala	Glu	Thr	Pro	
				325					330					335		
His	Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	
			340					345					350			
Glu	Asn	Phe	Cys	Gln	Thr	Gln	Met	Gly	Ile	Ala	Met	Gly	Pro	Gly	Ala	
		355					360					365				

Thr Arg Trp Thr Gln Gly Pro His Ser Thr Thr Val Pro Cys Asp Ala
 370 375 380
 Ala Leu Met Thr Ser Arg His Gln Ser Trp Thr Pro Gln Thr Arg Cys
 385 390 395 400
 Ser Leu Arg Ser Val Ala Arg Gly Trp Ile Gly Trp Ile Ser Val Val
 405 410 415
 Pro Ser Cys Ala Trp Leu Gly Ala Ile Arg Ala Thr His Pro Gly Gln
 420 425 430
 Ser Ala Cys Gly Ile Gly Gln Gly Gln His Phe Cys Gly Gly Ser Leu
 435 440 445
 Val Lys Glu Gln Trp Ile Leu Thr Ala Arg Gln Cys Phe Ser Ser Cys
 450 455 460
 His Met Pro Leu Thr Gly Tyr Glu Val Trp Leu Gly Thr Leu Phe Gln
 465 470 475 480
 Asn Pro Gln His Gly Glu Pro Gly Leu Gln Arg Val Pro Val Ala Lys
 485 490 495
 Met Leu Cys Gly Pro Ser Gly Ser Gln Leu Val Leu Leu Lys Leu Glu
 500 505 510
 Arg Ser Val Thr Leu Asn Gln Arg Val Ala Leu Ile Cys Leu Pro Pro
 515 520 525

Glu

<210> 55
 <211> 716
 <212> PRT
 <213> Mus musculus

<400> 55
 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Val Gln Cys Ser Arg Ala
 1 5 10 15
 Leu Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Leu Phe Arg Gly Thr
 20 25 30
 Glu Leu Arg Asn Leu Leu His Thr Ala Val Pro Gly Pro Trp Gln Glu
 35 40 45
 Asp Val Ala Asp Ala Glu Glu Cys Ala Arg Arg Cys Gly Pro Leu Leu
 50 55 60
 Asp Cys Arg Ala Phe His Tyr Asn Met Ser Ser His Gly Cys Gln Leu
 65 70 75 80
 Leu Pro Trp Thr Gln His Ser Leu His Thr Gln Leu Tyr His Ser Ser
 85 90 95

Leu	Cys	His	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met		
			100					105					110				
Asp	Asn	Gly	Val	Ser	Tyr	Arg	Gly	Thr	Val	Ala	Arg	Thr	Ala	Gly	Gly		
		115					120					125					
Leu	Pro	Cys	Gln	Ala	Trp	Ser	Arg	Arg	Phe	Pro	Asn	Asp	His	Lys	Tyr		
	130					135					140						
Thr	Pro	Thr	Pro	Lys	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro		
145					150					155					160		
Asp	Gly	Asp	Pro	Arg	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asn	Arg	Ser	Val		
				165					170					175			
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Thr	Cys	Arg	Glu	Ala	Val	Cys	Val		
			180					185					190				
Leu	Cys	Asn	Gly	Glu	Asp	Tyr	Arg	Gly	Glu	Val	Asp	Val	Thr	Glu	Ser		
	195						200				205						
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Ser	His	Pro		
	210					215					220						
Phe	Gln	Pro	Glu	Lys	Phe	Leu	Asp	Lys	Asp	Leu	Lys	Asp	Asn	Tyr	Cys		
225					230					235					240		
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro		
			245						250					255			
Asn	Val	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Ser	Cys	Gly	Pro	Asn	Leu		
		260						265					270				
Pro	Pro	Thr	Val	Lys	Gly	Ser	Lys	Ser	Gln	Arg	Arg	Asn	Lys	Gly	Lys		
		275					280					285					
Ala	Leu	Asn	Cys	Phe	Arg	Gly	Lys	Gly	Glu	Asp	Tyr	Arg	Gly	Thr	Thr		
	290					295					300						
Asn	Thr	Thr	Ser	Ala	Gly	Val	Pro	Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ser		
305					310					315					320		
Pro	His	Gln	His	Arg	Phe	Val	Pro	Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu		
				325					330					335			
Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys		
			340					345					350				
Phe	Thr	Ser	Arg	Pro	Gly	Leu	Arg	Met	Ala	Phe	Cys	His	Gln	Ile	Pro		
		355					360					365					
Arg	Cys	Thr	Glu	Glu	Leu	Val	Pro	Glu	Gly	Cys	Tyr	His	Gly	Ser	Gly		
	370					375					380						
Glu	Gln	Tyr	Arg	Gly	Ser	Val	Ser	Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys		
385					390					395					400		

Gln	His	Trp	Ser	Ser	Glu	Thr	Pro	His	Lys	Pro	Gln	Phe	Thr	Pro	Thr		
				405					410					415			
Ser	Ala	Pro	Gln	Ala	Gly	Leu	Glu	Ala	Asn	Phe	Cys	Arg	Asn	Pro	Asp		
			420					425					430				
Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	Pro	Asp	Ile	Leu		
		435					440					445					
Phe	Asp	Tyr	Cys	Ala	Leu	Gln	Arg	Cys	Asp	Asp	Asp	Gln	Pro	Pro	Ser		
	450					455					460						
Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Val	Phe	Glu	Lys	Cys	Gly	Lys	Arg		
465					470					475					480		
Val	Asp	Lys	Ser	Asn	Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn		
				485					490					495			
Ser	Pro	Trp	Thr	Val	Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys		
			500					505					510				
Gly	Gly	Ser	Leu	Val	Lys	Glu	Gln	Trp	Val	Leu	Thr	Ala	Arg	Gln	Cys		
		515					520					525					
Ile	Trp	Ser	Cys	His	Glu	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly		
	530					535					540						
Thr	Ile	Asn	Gln	Asn	Pro	Gln	Pro	Gly	Glu	Ala	Asn	Leu	Gln	Arg	Val		
545				550					555						560		
Pro	Val	Ala	Lys	Ala	Val	Cys	Gly	Pro	Ala	Gly	Ser	Gln	Leu	Val	Leu		
			565					570					575				
Leu	Lys	Leu	Glu	Arg	Pro	Val	Ile	Leu	Asn	His	His	Val	Ala	Leu	Ile		
		580					585					590					
Cys	Leu	Pro	Pro	Glu	Gln	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu		
	595					600					605						
Ile	Ala	Gly	Trp	Gly	Glu	Ser	Ile	Gly	Thr	Ser	Asn	Asn	Thr	Val	Leu		
	610					615					620						
His	Val	Ala	Ser	Met	Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Thr	Lys		
625				630					635						640		
Tyr	Arg	Gly	His	Ile	Gln	Glu	Ser	Glu	Ile	Cys	Thr	Gln	Gly	Leu	Val		
			645					650						655			
Val	Pro	Val	Gly	Ala	Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys		
		660					665					670					
Tyr	Thr	His	Asp	Cys	Trp	Val	Leu	Gln	Gly	Leu	Ile	Ile	Pro	Asn	Arg		
	675					680					685						
Val	Cys	Ala	Arg	Pro	Arg	Trp	Pro	Ala	Ile	Phe	Thr	Arg	Val	Ser	Val		
	690				695						700						

Phe Val Asp Trp Ile Asn Lys Val Met Gln Leu Glu
 705 710 715

<210> 56
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
 1 5 10 15
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30
 Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Val Thr Cys Asp
 35 40 45
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60
 Phe Ser Cys Pro Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
 85 90 95
 His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
 100 105 110
 Asp Gly Lys Leu Val Val Glu Cys Val Met Asn His Val Ala Cys Thr
 115 120 125
 Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 57
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 57
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
 1 5 10 15
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30
 Arg Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60

Phe Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
 85 90 95
 His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys
 100 105 110
 Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr
 115 120 125
 Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 58
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser
 1 5 10 15
 Arg Gly Phe Asp Glu Tyr Val Lys Glu Leu Gly Val Gly Ile Ala Leu
 20 25 30
 Arg Lys Met Asp Thr Ile Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp
 35 40 45
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln
 50 55 60
 Phe Ser Cys Thr Leu Gly Glu Asn Phe Glu Glu Thr Thr Ala Asp Gly
 65 70 75 80
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln
 85 90 95
 His Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Arg Arg Lys Leu Lys
 100 105 110
 Asp Gly Lys Leu Val Val Asp Cys Val Met Asn Ser Val Thr Cys Thr
 115 120 125
 Arg Ile Tyr Glu Lys Val Glu
 130 135

<210> 59
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Leu Asp Ser

1	5	10	15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu	20	25	30
Gln Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp	35	40	45
Gly Arg Asn Leu Thr Thr Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln	50	55	60
Phe Ser Cys Thr Leu Gly Asp Glu Phe Glu Glu Thr Thr Ala Asp Gly	65	70	75
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln	85	90	95
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys	100	105	110
Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr	115	120	125
Arg Ile Tyr Glu Lys Val Glu	130	135	

<210> 60

<211> 135

<212> PRT

<213> Bos taurus

<400> 60

Met Ala Thr Val Gln Gln Leu Val Gly Arg Trp Arg Leu Val Glu Ser	1	5	10	15
Lys Gly Phe Asp Glu Tyr Met Lys Glu Val Gly Val Gly Met Ala Leu	20	25	30	
Arg Lys Val Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Ser Asp	35	40	45	
Gly Lys Asn Leu Ser Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln	50	55	60	
Phe Ser Cys Lys Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly	65	70	75	80
Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln	85	90	95	
His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Glu	100	105	110	
Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr	115	120	125	

Arg Val Tyr Glu Lys Val Glu
 130 135

<210> 61
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 61

Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15

Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
 35 40 45

Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
 50 55 60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn
 100 105 110

Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
 115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly
 130 135 140

Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg
 145 150 155 160

Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr
 165 170 175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr
 180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Phe Tyr Leu
 195 200 205

Val Gly Lys Arg Cys Met Glu Ile Phe Gly Pro Arg His Arg Arg Pro
 210 215 220

Arg Cys Arg Glu Cys Leu Pro Asp Thr Cys Pro Pro Tyr Val Leu Ser
 225 230 235 240

Gln Gly Gly His Pro Glu Asp Gly Asn Ser Val Leu Met Lys Ala Gly
 245 250 255

Ser Ala Pro Val Asp Ala Gly Gly Tyr Pro
 260 265

<210> 62
 <211> 265
 <212> PRT
 <213> Rattus norvegicus

<400> 62

Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr
 1 5 10 15

Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg
 20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln
 35 40 45

Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys
 50 55 60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
 65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
 85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asp
 100 105 110

Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp
 115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly
 130 135 140

Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg
 145 150 155 160

Val Val Ala Cys Ser Val Gln Pro Cys Pro His Thr Val Asp Cys Tyr
 165 170 175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val
 180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Ala Tyr Leu
 195 200 205

Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Gln Lys Thr
 210 215 220

Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser
 225 230 235 240

Lys Gly His Pro Gln Asp Glu Ser Thr Val Leu Thr Lys Ala Gly Met

	245	250	255
Ala Thr Val Asp	Ala Gly Val Tyr Pro		
260	265		
<210> 63			
<211> 266			
<212> PRT			
<213> Mus musculus			
<400> 63			
Met Asn Trp Gly Phe Leu Gln Gly Ile Leu Ser Gly Val Asn Lys Tyr			
1	5	10	15
Ser Thr Ala Leu Gly Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg			
20	25	30	
Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Asp Gln			
35	40	45	
Lys Asp Phe Ile Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys			
50	55	60	
Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln			
65	70	75	80
Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala			
85	90	95	
Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asn			
100	105	110	
Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp			
115	120	125	
Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly			
130	135	140	
Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg			
145	150	155	160
Val Val Ala Cys Ser Val Thr Pro Cys Pro His Thr Val Asp Cys Tyr			
165	170	175	
Ile Ala Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val			
180	185	190	
Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Val Tyr Leu			
195	200	205	
Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Arg Lys Ala			
210	215	220	
Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser			
225	230	235	240

Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly
245 250 255

Met Ala Thr Val Asp Ala Gly Val Tyr Pro
260 265

<210> 64

<211> 273

<212> PRT

<213> Homo sapiens

<400> 64

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Glu Arg Val Trp Ser Asp Asp His
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Val Glu Leu Ile Tyr Leu
195 200 205

Val Ser Lys Arg Cys His Glu Cys Leu Ala Ala Arg Lys Ala Gln Ala
210 215 220

Met Cys Thr Gly His His Pro His Gly Thr Thr Ser Ser Cys Lys Gln
225 230 235 240

Asp Asp Leu Leu Ser Gly Asp Leu Ile Phe Leu Gly Ser Asp Ser His
245 250 255

Pro Pro Leu Leu Pro Asp Arg Pro Arg Asp His Val Lys Lys Thr Ile
260 265 270

Leu

<210> 65

<211> 273

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (41)

<223> Wherein Xaa is any amino acid.

<400> 65

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg
20 25 30

Val Leu Val Tyr Leu Val Thr Ala Xaa Arg Val Trp Ser Asp Asp His
35 40 45

Lys Asp Phe Asp Cys Asn Thr Arg Gln Pro Gly Cys Ser Asn Val Cys
50 55 60

Phe Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala
85 90 95

Tyr Arg Glu Val Gln Glu Lys Arg His Arg Glu Ala His Gly Glu Asn
100 105 110

Ser Gly Arg Leu Tyr Leu Asn Pro Gly Lys Lys Arg Gly Gly Leu Trp
115 120 125

Trp Thr Tyr Val Cys Ser Leu Val Phe Lys Ala Ser Val Asp Ile Ala
130 135 140

Phe Leu Tyr Val Phe His Ser Phe Tyr Pro Lys Tyr Ile Leu Pro Pro
145 150 155 160

Val Val Lys Cys His Ala Asp Pro Cys Pro Asn Ile Val Asp Cys Phe
165 170 175

Ile Ser Lys Pro Ser Glu Lys Asn Ile Phe Thr Leu Phe Met Val Ala
180 185 190

Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
	195						200					205			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	210					215					220				
Met	Cys	Thr	Gly	His	His	Pro	His	Gly	Thr	Thr	Ser	Ser	Cys	Lys	Gln
225					230					235					240
Asp	Asp	Leu	Leu	Ser	Gly	Asp	Leu	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
				245					250					255	
Pro	Pro	Leu	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
		260						265					270		

Leu

<210> 66
 <211> 434
 <212> PRT
 <213> Homo sapiens

<400> 66

Ala	Lys	Gln	Gln	Leu	Asn	Leu	Arg	Thr	His	Met	Ala	Asp	Glu	Asn	Lys
1				5					10					15	
Asn	Glu	Tyr	Ala	Ala	Gln	Leu	Gln	Asn	Phe	Asn	Gly	Glu	Gln	His	Lys
			20					25					30		
His	Phe	Tyr	Val	Val	Ile	Pro	Gln	Ile	Tyr	Lys	Gln	Leu	Gln	Glu	Met
		35					40					45			
Asp	Glu	Arg	Arg	Thr	Ile	Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe	Ala
	50					55					60				
Asp	Ser	Glu	Arg	Lys	Val	Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu	Gly
65					70					75					80
Met	Ile	Leu	Ala	Ala	Lys	Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln	Met
				85					90					95	
Val	Val	Asp	Ser	Phe	Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	Pro
			100					105					110		
Phe	Glu	Asp	Tyr	Ser	Gln	His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly	Thr
		115					120					125			
Ile	Ser	Ala	Ser	Lys	Gln	Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	Thr
		130				135					140				
Val	Gly	Lys	Ala	Lys	Gly	Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	Lys
145					150					155					160
Pro	Gln	Ser	Pro	Pro	Leu	Thr	Pro	Thr	Ser	Leu	Phe	Thr	Ser	Ser	Thr

165								170				175				
Pro	Asn	Gly	Ser	Gln	Phe	Leu	Thr	Phe	Ser	Ile	Glu	Pro	Val	His	Tyr	
			180							185			190			
Cys	Met	Asn	Glu	Ile	Lys	Thr	Gly	Lys	Pro	Arg	Ile	Pro	Ser	Phe	Arg	
		195					200					205				
Ser	Leu	Lys	Arg	Gly	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	Leu	Pro	
	210					215				220						
Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Asn	
225					230					235					240	
Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	Lys	Met	
				245					250					255		
Lys	Asp	Val	Tyr	Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu	
			260						265				270			
Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met	
		275					280					285				
Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr	
	290					295				300						
Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val	
305					310					315					320	
Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn	
				325					330					335		
Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe	
			340						345				350			
Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys	
		355					360					365				
Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met	
	370					375				380						
Lys	Glu	Gly	Glu	Val	Leu	Tyr	Ile	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	
385					390				395						400	
Trp	Thr	Arg	Ala	Arg	Arg	Gln	Asn	Gly	Glu	Glu	Gly	Tyr	Val	Pro	Thr	
				405					410					415		
Ser	Tyr	Ile	Asp	Val	Thr	Leu	Glu	Lys	Asn	Ser	Lys	Gly	Ala	Val	Thr	
			420						425				430			

Tyr Ile

<210> 67
 <211> 330
 <212> PRT

<213> Homo sapiens

<400> 67

Met	Asp	Glu	Arg	Arg	Thr	Ile	Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe
1				5					10					15	
Ala	Asp	Ser	Glu	Arg	Lys	Val	Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu
			20					25					30		
Gly	Met	Ile	Leu	Ala	Ala	Lys	Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln
		35					40					45			
Met	Val	Val	Asp	Ser	Phe	Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe
	50					55					60				
Pro	Phe	Glu	Asp	Tyr	Ser	Gln	His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly
65					70					75					80
Thr	Ile	Ser	Ala	Ser	Lys	Gln	Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr
				85					90					95	
Thr	Val	Gly	Lys	Ala	Lys	Gly	Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro
			100					105					110		
Lys	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg
		115					120					125			
Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Asn	Arg	Glu	Leu	Gln
	130					135					140				
Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	Lys	Met	Lys	Asp	Val	Tyr
145					150					155					160
Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu	Gln	Pro	Lys	Leu
				165					170					175	
Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met	Glu	Ile	His	Lys
			180					185					190		
Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr	Gly	Gly	Arg	Gly
	195						200					205			
Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val	Thr	Gln	Gly	Arg
	210					215					220				
Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn	Gln	Glu	Val	Arg
225					230					235					240
Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe	Asp	Asp	Glu	Phe
			245						250					255	
Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys	Lys	Ala	Ile	Tyr
			260					265					270		
Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met	Lys	Glu	Gly	Glu
		275					280					285			

Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala
 290 295 300

Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp
 305 310 315 320

Val Thr Leu Glu Lys Asn Ser Lys Gly Ser
 325 330

<210> 68

<211> 592

<212> PRT

<213> Homo sapiens

<400> 68

Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys
 1 5 10 15

His Thr Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val
 20 25 30

Lys Glu Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn
 35 40 45

Leu Ser Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu
 50 55 60

Tyr Lys Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met
 65 70 75 80

Asn Asp Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser
 85 90 95

Gln Ile Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu
 100 105 110

Arg Lys Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu
 115 120 125

Thr Cys Trp Lys Gln Leu Glu Ser Ser Lys Arg Arg Phe Glu Arg Asp
 130 135 140

Cys Lys Glu Ala Asp Arg Ala Gln Gln Tyr Phe Glu Lys Met Asp Ala
 145 150 155 160

Asp Ile Asn Val Thr Lys Ala Asp Val Glu Lys Ala Arg Gln Gln Ala
 165 170 175

Gln Ile Arg His Gln Met Ala Glu Asp Ser Lys Ala Asp Tyr Ser Ser
 180 185 190

Ile Leu Gln Lys Phe Asn His Glu Gln His Glu Tyr Tyr His Thr His
 195 200 205

Ile Pro Asn Ile Phe Gln Lys Ile Gln Glu Met Glu Glu Arg Arg Ile
 210 215 220

Val	Arg	Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	
225					230					235					240	
Val	Ile	Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	
			245						250					255		
Glu	Ser	Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	
		260						265					270			
Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	
		275					280						285			
Gln	Pro	Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	
	290					295					300					
Gly	Glu	Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	
305					310					315					320	
Leu	Trp	Pro	Phe	Ile	Lys	Lys	Asn	Lys	Ser	Pro	Lys	Gln	Gln	Lys	Glu	
			325						330					335		
Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	
			340					345					350			
His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	
		355					360					365				
Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	
	370					375					380					
Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	
385					390					395					400	
Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	
			405						410					415		
Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	
			420					425					430			
Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	
		435					440					445				
Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro	Ala	Arg	Asn	Glu	Gln	Ala	
	450					455					460					
Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	
465					470					475					480	
Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	
			485						490					495		
Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	
		500						505					510			
Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	
		515					520					525				

Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly Thr Ile Ser Val Val Glu
 530 535 540
 Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr
 545 550 555 560
 Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr
 565 570 575
 Val Glu Val Cys Leu Asp Lys Asn Ala Lys Gly Ala Lys Thr Tyr Ile
 580 585 590

<210> 69
 <211> 679
 <212> PRT
 <213> Homo sapiens

<400> 69
 Leu Trp Asn Gly Gly Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg
 1 5 10 15
 Ser Cys Glu Pro Glu Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser
 20 25 30
 Arg Gly Ser Arg Gly Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu
 35 40 45
 Pro Arg Pro Pro Arg Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser
 50 55 60
 Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr
 65 70 75 80
 Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu
 85 90 95
 Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser
 100 105 110
 Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys
 115 120 125
 Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp
 130 135 140
 Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile
 145 150 155 160
 Ile Val Asp Leu Ala Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys
 165 170 175
 Ser Asn Phe His Asp Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys

180						185						190					
Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys		
195						200						205					
Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile		
210						215				220							
Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile		
225				230						235				240			
Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu		
			245					250						255			
Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro		
			260					265					270				
Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg		
275						280						285					
Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile		
290						295				300							
Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser		
305				310						315				320			
Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser		
			325					330					335				
Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro		
			340					345					350				
Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu		
355						360						365					
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp		
370						375				380							
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His		
385				390						395				400			
Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro		
			405					410					415				
Asn	Gly	Pro	Gln	Ser	Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg		
420						425						430					
Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser		
435						440						445					
Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe		
450				455						460							
Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val		
465				470				475						480			
Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala		

485								490					495				
Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp		
			500							505				510			
Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu		
		515					520					525					
Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val		
		530				535					540						
Glu	Gly	Arg	Leu	Pro	Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly		
545					550					555					560		
Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp		
				565					570					575			
Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	Gln	Ser	Gln	Glu	Ser		
			580					585					590				
Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	Glu	Phe	Asp	Asp	Glu		
		595					600					605					
Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	Leu	Tyr	Thr	Phe	Glu		
		610				615					620						
Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu	Gly	Glu	Thr	Leu	Tyr		
625					630					635					640		
Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ile	Arg	Arg	Asn		
				645					650					655			
Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr	Val	Glu	Val	Cys	Leu		
			660						665				670				
Asp	Lys	Asn	Ala	Lys	Asp	Ser											
			675														

<210> 70
 <211> 674
 <212> PRT
 <213> Homo sapiens

<400> 70
 Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu
 1 5 10 15
 Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly
 20 25 30
 Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg
 35 40 45
 Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu
 50 55 60

Trp	Asp	Gln	Phe	Asp	Asn	Leu	Glu	Lys	His	Thr	Gln	Trp	Gly	Ile	Asp	
65					70					75					80	
Ile	Leu	Glu	Lys	Tyr	Ile	Lys	Phe	Val	Lys	Glu	Arg	Thr	Glu	Ile	Glu	
				85					90					95		
Leu	Ser	Tyr	Ala	Lys	Gln	Leu	Arg	Asn	Leu	Ser	Lys	Lys	Tyr	Gln	Pro	
			100					105					110			
Lys	Lys	Asn	Ser	Lys	Glu	Glu	Glu	Glu	Tyr	Lys	Tyr	Thr	Ser	Cys	Lys	
		115					120					125				
Ala	Phe	Ile	Ser	Asn	Leu	Asn	Glu	Met	Asn	Asp	Tyr	Ala	Gly	Gln	His	
	130					135					140					
Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser	Gln	Ile	Ile	Val	Asp	Leu	Ala	
145					150					155					160	
Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys	Ser	Asn	Phe	His	Asp	
				165					170					175		
Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys	Trp	Lys	Gln	Leu	Glu	
			180					185					190			
Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	Glu	Ala	Asp	Arg	Ala	
		195					200					205				
Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	Asn	Val	Thr	Lys	Ala	
	210					215					220					
Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	Arg	His	Gln	Met	Ala	
225					230					235					240	
Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	Gln	Lys	Phe	Asn	His	
				245					250					255		
Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	Asn	Ile	Phe	Gln	Lys	
			260					265					270			
Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	Met	Gly	Glu	Ser	Met	
		275					280					285				
Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	Pro	Ile	Ile	Gly	Lys	
	290					295					300					
Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	Ile	Asp	Gln	Lys	Asn	
305					310					315					320	
Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	Gly	Phe	Glu	Pro	Pro	
				325					330					335		
Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	Met	Lys	Arg	Thr	Val	
			340					345					350			
Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	Gly	Lys	Pro	Asp	Leu	
		355					360					365				

Lys Phe Gly Gly Lys Ser Lys Gly Lys Leu Trp Pro Phe Ile Lys Lys
 370 375 380
 Asn Lys Leu Met Ser Leu Leu Thr Ser Pro His Gln Pro Pro Pro Pro
 385 390 395 400
 Pro Pro Ala Ser Ala Ser Pro Ser Ala Val Pro Asn Gly Pro Gln Ser
 405 410 415
 Pro Lys Gln Gln Lys Glu Pro Leu Ser His Arg Phe Asn Glu Phe Met
 420 425 430
 Thr Ser Lys Pro Lys Ile His Cys Phe Arg Ser Leu Lys Arg Gly Leu
 435 440 445
 Ser Leu Lys Leu Gly Ala Thr Pro Glu Asp Phe Ser Asn Leu Pro Pro
 450 455 460
 Glu Gln Arg Arg Lys Lys Leu Gln Gln Lys Val Asp Glu Leu Asn Lys
 465 470 475 480
 Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala Ile Thr Lys Met Lys
 485 490 495
 Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp Pro Ala Ser Leu Asp
 500 505 510
 His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu Lys Leu Arg Val Glu
 515 520 525
 Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val Glu Gly Arg Leu Pro
 530 535 540
 Ala Arg Ser Glu Gln Ala Arg Arg Gln Ser Gly Leu Tyr Asp Ser Gln
 545 550 555 560
 Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp Arg Glu Ser Pro Asp
 565 570 575
 Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser Glu Met Lys Val Leu
 580 585 590
 Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu Glu Pro Leu Pro Ala
 595 600 605
 Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu Gly Gln Asn Glu Gly
 610 615 620
 Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp
 625 630 635 640
 Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly
 645 650 655
 Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu Asp Lys Asn Ala Lys
 660 665 670

Asp Ser

<210> 71
<211> 457
<212> PRT
<213> Homo sapiens

<400> 71

Met	Ser	Leu	Met	Leu	Asp	Asp	Gln	Pro	Pro	Met	Glu	Ala	Gln	Tyr	Ala	
1				5					10						15	
Glu	Glu	Gly	Pro	Gly	Pro	Gly	Ile	Phe	Arg	Ala	Glu	Pro	Gly	Asp	Gln	
			20					25					30			
Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly	
		35					40					45				
Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly	
	50					55					60					
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile	
65					70					75					80	
Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala	
				85					90					95		
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe	
		100						105					110			
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln	
		115					120					125				
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly	
	130					135					140					
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys	
145					150					155					160	
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala	
			165						170					175		
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro	
		180						185					190			
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu	
	195						200					205				
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val	
	210					215					220					
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg	
225					230					235					240	
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala	
			245						250					255		

Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
 260 265 270
 Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
 275 280 285
 Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
 290 295 300
 His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
 305 310 315 320
 Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
 325 330 335
 Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
 340 345 350
 Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro Leu
 355 360 365
 Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala Leu
 370 375 380
 Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
 385 390 395 400
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Asp Gly Asp Thr
 405 410 415
 Trp Arg Leu Val Gly Val Val Ser Trp Gly Arg Ala Cys Ala Glu Pro
 420 425 430
 Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
 435 440 445
 His Asp Thr Ala Gln Asp Ser Leu Leu
 450 455

<210> 72

<211> 455

<212> PRT

<213> Mus musculus

<400> 72

Met Ser Pro Thr Leu Asp Asp Gln Ser Pro Met Glu Ile Arg Cys Thr
 1 5 10 15
 Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg Met Glu Leu Gly Asp Gln
 20 25 30
 Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp Cys Cys Leu Gln Arg Gly
 35 40 45
 Cys Val Ile Leu Gly Val Leu Gly Leu Leu Ala Gly Ala Gly Ile Ala

50					55					60					
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Trp	Pro	Ala	Ala	Ser	Pro	Ser	Ile
65					70					75					80
Ser	Gly	Thr	Leu	Gln	Glu	Glu	Glu	Met	Thr	Leu	Asn	Cys	Pro	Gly	Val
				85					90					95	
Ser	Cys	Glu	Glu	Glu	Leu	Leu	Pro	Ser	Leu	Pro	Lys	Thr	Val	Ser	Phe
			100				105						110		
Arg	Ile	Asn	Gly	Glu	Asp	Leu	Leu	Leu	Gln	Val	Gln	Val	Arg	Ala	Arg
		115				120						125			
Pro	Asp	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly
	130					135					140				
Met	His	Ile	Cys	Lys	Ser	Leu	Gly	His	Ile	Arg	Leu	Thr	Gln	His	Lys
145				150						155					160
Ala	Val	Asn	Leu	Ser	Asp	Ile	Lys	Leu	Asn	Arg	Ser	Gln	Glu	Phe	Ala
				165					170					175	
Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val	Glu	Glu	Ala	Trp	Lys	Pro
			180					185					190		
Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val	Ser	Leu	Lys	Cys	Ser	Glu
	195					200						205			
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ala	Val
	210					215					220				
Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Met	Leu	Gly	Ser	Arg
225				230						235					240
His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro	His	Trp	Val	Val	Thr	Ala
			245						250					255	
Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser	Arg	Leu	Ser	Ser	Trp	Arg
			260					265					270		
Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala	Val	Arg	Gln	His	Gln	Gly
		275					280					285			
Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn
	290					295					300				
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	Arg	Thr	Pro	Ile	Asn	Phe
305				310						315					320
Ser	Asp	Thr	Val	Asp	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	Tyr	Phe
			325						330					335	
Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	Asp	Pro
			340					345					350		
Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln	Asp	Thr	Met	Val	Pro	Leu

355 360 365
 Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu
 370 375 380
 Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
 385 390 395 400
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr
 405 410 415
 Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro
 420 425 430
 Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
 435 440 445
 His Asp Thr Val Gln Val Arg
 450 455

<210> 73
 <211> 445
 <212> PRT
 <213> Mus musculus

<400> 73
 Met Glu Ile Arg Cys Thr Glu Glu Gly Ala Gly Pro Gly Ile Phe Arg
 1 5 10 15
 Met Glu Leu Gly Asp Gln Arg Gln Ser Ile Ser Gln Ser Gln Arg Trp
 20 25 30
 Cys Cys Leu Gln Arg Gly Cys Val Ile Leu Gly Val Leu Gly Leu Leu
 35 40 45
 Ala Gly Ala Gly Ile Ala Ser Trp Leu Leu Val Leu Tyr Leu Trp Pro
 50 55 60
 Ala Ala Ser Pro Ser Ile Ser Gly Thr Leu Gln Glu Glu Glu Met Thr
 65 70 75 80
 Leu Asn Cys Pro Gly Val Ser Cys Glu Glu Glu Leu Leu Pro Ser Leu
 85 90 95
 Pro Lys Thr Val Ser Phe Arg Ile Asn Gly Glu Asp Leu Leu Leu Gln
 100 105 110
 Val Gln Val Arg Ala Arg Pro Asp Trp Leu Leu Val Cys His Glu Gly
 115 120 125
 Trp Ser Pro Ala Leu Gly Met His Ile Cys Lys Ser Leu Gly His Ile
 130 135 140
 Arg Leu Thr Gln His Lys Ala Val Asn Leu Ser Asp Ile Lys Leu Asn
 145 150 155 160

Arg Ser Gln Glu Phe Ala Gln Leu Ser Ala Arg Pro Gly Gly Leu Val
 165 170 175
 Glu Glu Ala Trp Lys Pro Ser Ala Asn Cys Pro Ser Gly Arg Ile Val
 180 185 190
 Ser Leu Lys Cys Ser Glu Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile
 195 200 205
 Val Gly Gly Gln Ala Val Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser
 210 215 220
 Val Met Leu Gly Ser Arg His Thr Cys Gly Ala Ser Val Leu Ala Pro
 225 230 235 240
 His Trp Val Val Thr Ala Ala His Cys Met Tyr Ser Phe Arg Leu Ser
 245 250 255
 Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly Ala
 260 265 270
 Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His Pro
 275 280 285
 Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln Leu
 290 295 300
 Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu Pro
 305 310 315 320
 Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser Gly
 325 330 335
 Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu Gln
 340 345 350
 Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser Cys
 355 360 365
 Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr Leu
 370 375 380
 Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 385 390 395 400
 Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp Gly
 405 410 415
 Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val Ala
 420 425 430
 Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg
 435 440 445

<210> 74
 <211> 398

<212> PRT

<213> Homo sapiens

<400> 74

Met	Ser	Leu	Met	Leu	Asp	Asp	Gln	Pro	Pro	Met	Glu	Ala	Gln	Tyr	Ala	
1				5					10					15		
Glu	Glu	Gly	Pro	Gly	Pro	Gly	Ile	Phe	Arg	Ala	Glu	Pro	Gly	Asp	Gln	
			20					25					30			
Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly	
		35					40					45				
Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly	
	50					55					60					
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile	
65					70				75						80	
Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala	
				85				90						95		
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe	
		100						105					110			
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln	
		115					120					125				
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly	
	130					135					140					
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys	
145					150				155						160	
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala	
			165					170						175		
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro	
			180					185					190			
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu	
		195					200					205				
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val	
	210					215					220					
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg	
225					230					235					240	
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala	
			245						250					255		
Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	Ala	Arg	Leu	Ser	Ser	Trp	Arg	
			260					265						270		
Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	Ala	Val	Arg	Pro	His	Gln	Gly	
		275					280					285				

Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
290 295 300

His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
305 310 315 320

Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
325 330 335

Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
340 345 350

Ser His Ser Leu Gln Leu Gly Tyr Ala Pro Gly His Gly Gly Ala Leu
355 360 365

Val Gln His Ser Ala Leu Gln Gln Leu Leu Arg Val Gln Arg Ser Pro
370 375 380

His Pro Pro His Ala Leu Arg Trp Leu Pro Gly Arg Lys Gly
385 390 395

<210> 75
<211> 311
<212> PRT
<213> Mus musculus

<400> 75
Met His Ile Cys Lys Ser Leu Gly His Ile Arg Leu Thr Gln His Lys
1 5 10 15

Ala Val Asn Leu Ser Asp Ile Lys Leu Asn Arg Ser Gln Glu Phe Ala
20 25 30

Gln Leu Ser Ala Arg Pro Gly Gly Leu Val Glu Glu Ala Trp Lys Pro
35 40 45

Ser Ala Asn Cys Pro Ser Gly Arg Ile Val Ser Leu Lys Cys Ser Glu
50 55 60

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ala Val
65 70 75 80

Ala Ser Gly Arg Trp Pro Trp Gln Ala Ser Val Met Leu Gly Ser Arg
85 90 95

His Thr Cys Gly Ala Ser Val Leu Ala Pro His Trp Val Val Thr Ala
100 105 110

Ala His Cys Met Tyr Ser Phe Arg Leu Ser Arg Leu Ser Ser Trp Arg
115 120 125

Val His Ala Gly Leu Val Ser His Gly Ala Val Arg Gln His Gln Gly
130 135 140

Thr Met Val Glu Lys Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn

145		150		155		160
His Asp Tyr Asp Val Ala Leu Leu Gln Leu Arg Thr Pro Ile Asn Phe						
	165			170		175
Ser Asp Thr Val Asp Ala Val Cys Leu Pro Ala Lys Glu Gln Tyr Phe						
	180			185		190
Pro Trp Gly Ser Gln Cys Trp Val Ser Gly Trp Gly His Thr Asp Pro						
	195			200		205
Ser His Thr His Ser Ser Asp Thr Leu Gln Asp Thr Met Val Pro Leu						
	210			215		220
Leu Ser Thr His Leu Cys Asn Ser Ser Cys Met Tyr Ser Gly Ala Leu						
	225			230		240
Thr His Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala						
	245			250		255
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Ser Gly Asp Thr						
	260			265		270
Trp His Leu Val Gly Val Val Ser Trp Gly Arg Gly Cys Ala Glu Pro						
	275			280		285
Asn Arg Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile						
	290			295		300
His Asp Thr Val Gln Val Arg						
	305			310		

<210> 76
 <211> 199
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Reprolysin
 family zinc protease Consensus Sequence

<400> 76
Lys Tyr Ile Glu Leu Phe Ile Val Val Asp His Gly Met Phe Thr Lys
1 5 10 15
Tyr Gly Ser Asp Leu Asn Lys Ile Arg Gln Arg Val His Gln Ile Val
20 25 30
Asn Leu Val Asn Glu Ile Tyr Arg Pro Leu Asn Ile Arg Val Val Leu
35 40 45
Val Gly Leu Glu Ile Trp Ser Asp Gly Asp Lys Ile Thr Val Gln Gly
50 55 60
Asp Ala Asn Asp Thr Leu His Arg Phe Leu Glu Trp Arg Glu Thr Asp
65 70 75 80

Leu Leu Lys Arg Lys Ser His Asp Asn Ala Gln Leu Leu Thr Gly Ile
 85 90 95
 Asp Phe Asp Gly Asn Thr Ile Gly Ala Ala Tyr Val Gly Gly Met Cys
 100 105 110
 Ser Pro Lys Arg Ser Val Gly Val Val Gln Asp His Ser Pro Ile Val
 115 120 125
 Leu Leu Val Ala Val Thr Met Ala His Glu Leu Gly His Asn Leu Gly
 130 135 140
 Met Thr His Asp Asp Ile Asn Lys Cys Thr Cys Glu Gly Gly Gly Gly
 145 150 155 160
 Cys Ile Met Asn Pro Val Ala Ser Ser Ser Pro Gly Lys Lys Phe Ser
 165 170 175
 Asn Cys Ser Met Asp Asp Tyr Gln Gln Phe Leu Thr Lys Gly Lys Pro
 180 185 190
 Gln Cys Leu Leu Asn Lys Pro
 195

<210> 77
 <211> 51
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Thrombospondin
 type 1 Consensus Sequence

<400> 77
 Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly
 1 5 10 15
 Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly
 20 25 30
 Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln
 35 40 45
 Pro Cys Pro
 50

<210> 78
 <211> 48
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Thrombospondin
 type 1 domain Consensus Sequence

<400> 78

Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly
1 5 10 15

Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro
20 25 30

Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys
35 40 45

<210> 79

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reprolysin
family propeptide Consensus Sequence

<400> 79

His Leu Glu Lys Asn Arg Ser Leu Leu Ala Pro Asp Phe Thr Val Thr
1 5 10 15

Thr Tyr Asp Asp Asp Gly Thr Leu Val Thr Glu His Pro Leu Ile Gln
20 25 30

Asp His Cys Tyr Tyr Gln Gly Tyr Val Glu Gly Tyr Pro Asn Ser Ala
35 40 45

Val Ser Leu Ser Thr Cys Ser Gly Leu Arg Gly Ile Leu Gln Leu Glu
50 55 60

Asn Leu Ser Tyr Gly Ile Glu Pro Leu Glu Ser Ser Asp Gly Phe Glu
65 70 75 80

His Ile Ile Tyr Gln Ile Glu His Leu Lys Thr Val Pro Gly Pro Cys
85 90 95

Gly Glu Cys Gly Ser Leu Ser Val Ser Thr Asp Ser Gln Tyr Gly Ile
100 105 110

Arg Ser Pro Ser Pro
115

<210> 80

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Alpha-2-macroglobulin family Consensus Sequence

<400> 80

Ile	Asp	Glu	Asp	Asp	Ile	Thr	Ile	Arg	Ser	Tyr	Phe	Pro	Glu	Ser	Trp	1	5	10	15
Leu	Trp	Glu	Val	Glu	Glu	Val	Asp	Arg	Ser	Pro	Val	Leu	Thr	Val	Asn	20	25	30	
Ile	Thr	Leu	Pro	Asp	Ser	Ile	Thr	Thr	Trp	Glu	Ile	Leu	Ala	Val	Ser	35	40	45	
Leu	Ser	Asn	Thr	Lys	Gly	Leu	Cys	Val	Ala	Asp	Pro	Val	Glu	Leu	Thr	50	55	60	
Val	Phe	Gln	Asp	Phe	Phe	Leu	Glu	Leu	Arg	Leu	Pro	Tyr	Ser	Val	Val	65	70	75	80
Arg	Gly	Glu	Gln	Val	Glu	Leu	Arg	Ala	Val	Leu	Tyr	Asn	Tyr	Leu	Pro	85	90	95	
Ser	Gln	Asp	Ile	Lys	Val	Val	Val	Gln	Leu	Glu	Val	Glu	Pro	Leu	Cys	100	105	110	
Gln	Ala	Gly	Phe	Cys	Ser	Leu	Ala	Thr	Gln	Arg	Thr	Arg	Ser	Ser	Gln	115	120	125	
Ser	Val	Arg	Pro	Lys	Ser	Leu	Ser	Ser	Val	Ser	Phe	Pro	Val	Val	Val	130	135	140	
Val	Pro	Leu	Ala	Ser	Gly	Leu	Ser	Leu	Val	Glu	Val	Val	Ala	Ser	Val	145	150	155	160
Pro	Glu	Phe	Phe	Val	Lys	Asp	Ala	Val	Val	Lys	Thr	Leu	Lys	Val	Glu	165	170	175	
Pro	Glu	Gly	Ala	Arg	Lys	Glu	Glu	Thr	Val	Ser	Ser	Leu	Leu	Leu	Pro	180	185	190	
Pro	Glu	His	Leu	Gly	Gly	Gly	Leu	Glu	Val	Ser	Glu	Val	Pro	Ala	Leu	195	200	205	
Lys	Leu	Pro	Asp	Asp	Val	Pro	Asp	Thr	Glu	Ala	Glu	Ala	Val	Ile	Ser	210	215	220	
Val	Gln	Gly	Asp	Pro	Val	Ala	Gln	Ala	Ile	Gln	Asn	Thr	Leu	Ser	Gly	225	230	235	240
Glu	Gly	Leu	Asn	Asn	Leu	Leu	Arg	Leu	Pro	Ser	Gly	Cys	Gly	Glu	Gln	245	250	255	
Asn	Met	Ile	Tyr	Met	Ala	Pro	Thr	Val	Tyr	Val	Leu	His	Tyr	Leu	Asp	260	265	270	
Glu	Thr	Trp	Gln	Trp	Glu	Lys	Pro	Gly	Thr	Lys	Lys	Lys	Gln	Lys	Ala	275	280	285	

Ile	Asp	Leu	Ile	Asn	Lys	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Arg	Lys	290	295	300	
Ala	Asp	Gly	Ser	Tyr	Ala	Ala	Phe	Leu	His	Arg	Ala	Ser	Ser	Thr	Trp	305	310	315	320
Leu	Thr	Ala	Phe	Val	Leu	Lys	Val	Phe	Ser	Gln	Ala	Arg	Asn	Tyr	Val	325	330	335	
Phe	Ile	Asp	Glu	Glu	His	Ile	Cys	Gly	Ala	Val	Lys	Trp	Leu	Ile	Leu	340	345	350	
Asn	Gln	Gln	Lys	Asp	Asp	Gly	Val	Phe	Arg	Glu	Ser	Gly	Pro	Val	Ile	355	360	365	
His	Asn	Glu	Met	Lys	Gly	Gly	Val	Gly	Asp	Asp	Ala	Glu	Val	Glu	Val	370	375	380	
Thr	Leu	Thr	Ala	Phe	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ala	Lys	Leu	Val	385	390	395	400
Cys	Ile	Ser	Pro	Val	Val	Ala	Asn	Ala	Leu	Ser	Ile	Leu	Lys	Ala	Ser	405	410	415	
Asp	Tyr	Leu	Leu	Glu	Asn	Tyr	Ala	Asn	Gly	Gln	Arg	Val	Tyr	Thr	Leu	420	425	430	
Ala	Leu	Thr	Ala	Tyr	Ala	Leu	Ala	Leu	Ala	Gly	Val	Leu	His	Lys	Leu	435	440	445	
Lys	Glu	Ile	Leu	Lys	Ser	Leu	Lys	Glu	Glu	Leu	Tyr	Lys	Ala	Leu	Val	450	455	460	
Lys	Gly	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Asp	Ala	Pro	Gly	His	465	470	475	480
Pro	Tyr	Ser	Pro	Gln	Pro	Gln	Ala	Ala	Ala	Val	Glu	Met	Thr	Ser	Tyr	485	490	495	
Ala	Leu	Leu	Ala	Leu	Leu	Thr	Leu	Leu	Pro	Phe	Pro	Lys	Val	Glu	Met	500	505	510	
Ala	Pro	Lys	Val	Val	Lys	Trp	Leu	Thr	Glu	Gln	Gln	Tyr	Tyr	Gly	Gly	515	520	525	
Gly	Phe	Gly	Ser	Thr	Gln	Asp	Thr	Val	Met	Ala	Leu	Gln	Ala	Leu	Ser	530	535	540	
Lys	Tyr	Gly	Ile	Ala	Thr	Pro	Thr	His	Lys	Glu	Lys	Asn	Leu	Ser	Val	545	550	555	560
Thr	Ile	Gln	Ser	Pro	Ser	Gly	Ser	Phe	Lys	Ser	His	Phe	Gln	Ile	Leu	565	570	575	
Asn	Asn	Asn	Ala	Phe	Leu	Leu	Arg	Pro	Val	Glu	Leu	Pro	Leu	Asn	Glu	580	585	590	

Gly Phe Thr Val Thr Ala Lys Val Thr Gly Gln Gly Thr Leu Thr Leu
 595 600 605
 Val Thr Thr Tyr Arg Tyr Lys Val Leu Asp Lys Lys Asn Thr Phe Cys
 610 615 620
 Phe Asp Leu Lys Ile Glu Thr Val Pro Asp Thr Cys Val Glu Pro Lys
 625 630 635 640
 Gly Ala Lys Asn Ser Asp Tyr Leu Ser Ile Cys Thr Arg Tyr Ala Gly
 645 650 655
 Ser Arg Ser Asp Ser Gly Met Ala Ile Ala Asp Ile Ser Met Leu Thr
 660 665 670
 Gly Phe Ile Pro Leu Lys Pro Asp Leu Lys Lys Leu Glu Asn Gly Val
 675 680 685
 Asp Arg Tyr Val Ser Lys Tyr Glu Ile Asp Gly Asn His Val Leu Leu
 690 695 700
 Tyr Leu Asp Lys Val Ser His Ser Glu Thr Glu Cys Val Gly Phe Lys
 705 710 715 720
 Ile His Gln Asp Phe Glu Val Gly Leu Leu Gln Pro Ala Ser Val Lys
 725 730 735
 Val Tyr Asp Tyr Tyr Glu Pro Asp Glu Gln Cys Thr Ala Phe Tyr
 740 745 750

<210> 81
 <211> 620
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Alpha-2-macroglobulin family N-terminal region
 Consensus Sequence

<400> 81
 Arg Leu Leu Trp Leu Leu Leu Leu Leu Leu Phe Phe Asp Ser Ser
 1 5 10 15
 Leu Gln Lys Pro Arg Tyr Met Val Ile Val Pro Ser Ile Leu Arg Thr
 20 25 30
 Glu Thr Pro Glu Lys Val Cys Val Gln Leu His Asp Leu Asn Glu Thr
 35 40 45
 Val Thr Val Thr Val Ser Leu His Ser Phe Pro Gly Lys Arg Asn Leu
 50 55 60
 Ser Ser Leu Phe Thr Val Leu Leu Ser Ser Lys Asp Leu Phe His Cys
 65 70 75 80

Val	Ser	Phe	Thr	Val	Pro	Gln	Pro	Gly	Leu	Phe	Lys	Ser	Ser	Lys	Gly	85	90	95
Glu	Glu	Ser	Phe	Val	Val	Val	Gln	Val	Lys	Gly	Pro	Thr	His	Thr	Phe	100	105	110
Lys	Glu	Lys	Val	Thr	Val	Leu	Val	Ser	Ser	Arg	Arg	Gly	Leu	Val	Phe	115	120	125
Ile	Gln	Thr	Asp	Lys	Pro	Ile	Tyr	Thr	Pro	Gly	Gln	Thr	Val	Arg	Tyr	130	135	140
Arg	Val	Phe	Ser	Val	Asp	Glu	Asn	Leu	Arg	Pro	Leu	Asn	Glu	Leu	Ile	145	150	155
Leu	Val	Tyr	Ile	Glu	Asp	Pro	Glu	Gly	Asn	Arg	Val	Asp	Gln	Trp	Glu	165	170	175
Val	Asn	Lys	Leu	Glu	Gly	Gly	Ile	Phe	Gln	Leu	Ser	Phe	Pro	Ile	Pro	180	185	190
Ser	Glu	Pro	Ile	Gln	Gly	Thr	Trp	Lys	Ile	Val	Ala	Arg	Tyr	Glu	Ser	195	200	205
Gly	Pro	Glu	Ser	Asn	Tyr	Thr	His	Tyr	Phe	Glu	Val	Lys	Glu	Tyr	Val	210	215	220
Leu	Pro	Ser	Phe	Glu	Val	Ser	Ile	Thr	Pro	Pro	Lys	Pro	Phe	Ile	Tyr	225	230	235
Tyr	Asp	Asn	Phe	Lys	Glu	Phe	Glu	Val	Thr	Ile	Cys	Ala	Arg	Tyr	Thr	245	250	255
Tyr	Gly	Lys	Pro	Val	Pro	Gly	Val	Ala	Tyr	Val	Arg	Phe	Gly	Val	Lys	260	265	270
Asp	Glu	Asp	Gly	Lys	Lys	Glu	Leu	Leu	Ala	Gly	Leu	Glu	Glu	Arg	Ala	275	280	285
Lys	Leu	Leu	Asp	Gly	Asn	Gly	Glu	Ile	Cys	Leu	Ser	Gln	Glu	Val	Leu	290	295	300
Leu	Lys	Glu	Leu	Gln	Leu	Lys	Asn	Glu	Asp	Leu	Glu	Gly	Lys	Ser	Leu	305	310	315
Tyr	Val	Ala	Val	Ala	Val	Ile	Glu	Ser	Glu	Gly	Gly	Asp	Met	Glu	Glu	325	330	335
Ala	Glu	Leu	Gly	Gly	Ile	Lys	Ile	Val	Arg	Ser	Pro	Tyr	Lys	Leu	Lys	340	345	350
Phe	Val	Lys	Thr	Pro	Ser	His	Phe	Lys	Pro	Gly	Ile	Pro	Phe	Phe	Leu	355	360	365
Lys	Val	Leu	Val	Val	Asp	Pro	Asp	Gly	Ser	Pro	Ala	Pro	Asn	Val	Pro	370	375	380

Val Lys Val Ser Ala Gln Asp Ala Ser Tyr Tyr Ser Asn Gly Thr Thr
 385 390 395 400
 Asp Glu Asp Gly Leu Ala Gln Phe Ser Ile Asn Thr Ser Gly Ile Ser
 405 410 415
 Ser Leu Ser Ile Thr Val Arg Thr Asn His Lys Glu Leu Pro Glu Glu
 420 425 430
 Val Gln Ala His Ala Glu Ala Gln Ala Thr Ala Tyr Ser Thr Val Ser
 435 440 445
 Leu Ser Lys Ser Tyr Ile His Leu Ser Ile Glu Arg Thr Leu Pro Cys
 450 455 460
 Gly Pro Gly Val Gly Glu Gln Ala Asn Phe Ile Leu Arg Gly Lys Ser
 465 470 475 480
 Leu Gly Glu Leu Lys Ile Leu His Phe Tyr Tyr Leu Ile Met Ser Lys
 485 490 495
 Gly Lys Ile Val Lys Thr Gly Arg Glu Pro Arg Glu Pro Gly Gln Gly
 500 505 510
 Leu Phe Ser Leu Ser Ile Pro Val Thr Pro Asp Leu Ala Pro Ser Phe
 515 520 525
 Arg Leu Val Ala Tyr Tyr Ile Leu Pro Gln Gly Glu Val Val Ala Asp
 530 535 540
 Ser Val Trp Ile Asp Val Glu Asp Cys Cys Ala Asn Lys Leu Asp Leu
 545 550 555 560
 Ser Phe Ser Pro Ser Lys Asp Tyr Arg Leu Pro Ala Gln Gln Val Lys
 565 570 575
 Leu Arg Val Glu Ala Asp Pro Gln Ser Leu Val Ala Leu Arg Ala Val
 580 585 590
 Asp Gln Ala Val Tyr Leu Leu Lys Pro Lys Ala Lys Leu Ser Met Ser
 595 600 605
 Lys Val Tyr Asp Leu Leu Glu Lys Ser Asp Leu Gly
 610 615 620

<210> 82

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sodium Bile
acid symporter family consensus sequence

<400> 82

Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg

1	5	10	15
Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu	20	25	30
Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu	35	40	45
Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile	50	55	60
Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr	65	70	75
Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser	85	90	95
Thr Leu Leu Ala Pro Leu Val Thr Pro Leu Leu Ser Phe Leu Leu Ala	100	105	110
Gly Leu Leu Val His Val Asp Ala Val Ser Pro Trp Ser Leu Ile Lys	115	120	125
Ser Val Leu Val Tyr Val Ile Ile Pro Leu Ile Ala Gly Met Leu Thr	130	135	140
Arg Tyr Phe Leu Pro Glu Trp Phe Glu Gln Arg Val Leu Pro Val Leu	145	150	155
Ser Pro Ile Ser Leu Ile Gly Leu Leu Leu Thr Ile Val Val Ile Phe	165	170	175
Ala Leu Asn Gly Glu Val Ile Ala Ser Leu	180	185	

<210> 83

<211> 191

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SPFH
domain/Band 7 family Consensus Sequence

<400> 83

Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val	1	5	10	15
Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg	20	25	30	
Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe	35	40	45	
Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val	50	55	60	

Pro Ser Gln Glu Ile Ile Thr Lys Asp Asn Val Val Val Ile Val Asp
 65 70 75 80
 Ala Val Val Tyr Tyr Arg Val Val Asp Pro Leu Lys Ala Val Tyr Glu
 85 90 95
 Val Glu Asp Ala Glu Arg Ala Leu Pro Gln Leu Ala Gln Thr Thr Leu
 100 105 110
 Arg Asn Val Ile Gly Gln Phe Thr Leu Asp Glu Ile Leu Thr Glu Arg
 115 120 125
 Glu Arg Ile Asn Ser Gln Leu Arg Glu Ile Leu Asp Glu Ala Thr Asp
 130 135 140
 Pro Trp Gly Ile Lys Val Glu Arg Val Glu Ile Lys Asp Ile Arg Leu
 145 150 155 160
 Pro Glu Glu Val Gln Arg Ala Met Ala Ala Gln Met Glu Ala Glu Arg
 165 170 175
 Glu Ala Arg Ala Lys Ile Leu Glu Ala Glu Gly Glu Gln Glu Ala
 180 185 190

<210> 84

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Prohibitin
homologues Consensus Sequence

<400> 84

Ala Ala Phe Tyr Val Ile Gly Glu Gly Glu Arg Gly Val Val Glu Arg
 1 5 10 15
 Leu Gly Arg Val Leu Lys Val Leu Gly Pro Gly Leu His Phe Val Ile
 20 25 30
 Pro Phe Ile Asp Asp Val Lys Arg Val Asp Leu Arg Ala Gln Thr Asp
 35 40 45
 Asp Val Pro Pro Gln Glu Val Ile Thr Lys Asp Asn Val Thr Val Ser
 50 55 60
 Val Asp Ala Val Val Tyr Tyr Arg Val Leu Asp Pro Leu Lys Ala Val
 65 70 75 80
 Tyr Gly Val Leu Asp Ala Asp Tyr Arg Ala Leu Arg Gln Leu Ala Gln
 85 90 95
 Thr Thr Leu Arg Ser Val Ile Gly Lys Arg Thr Leu Asp Glu Leu Leu
 100 105 110

Thr Asp Glu Arg Glu Lys Ile Ser Glu Asn Ile Arg Glu Glu Leu Asn
115 120 125

Glu Ala Ala Glu Pro Trp Gly Ile Glu Val Glu Asp Val Glu Ile Lys
130 135 140

Asp Ile Arg Leu Pro Glu Glu Ile Lys Glu Ala Met Glu Ala Gln Gln
145 150 155 160

<210> 85

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 85

Cys Tyr His Gly Asn Gly Glu Asn Tyr Arg Gly Thr Ala Ser Thr Thr
1 5 10 15

Glu Ser Gly Ala Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro His Arg
20 25 30

His Ser Lys Tyr Thr Pro Glu Arg Tyr Pro Ala Lys Gly Leu Gly Glu
35 40 45

Asn Tyr Cys Arg Asn Pro Asp Gly Asp Glu Arg Pro Trp Cys Tyr Thr
50 55 60

Thr Asp Pro Arg Val Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys
65 70 75

<210> 86

<211> 83

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Kringle domain
Consensus Sequence

<400> 86

Arg Asp Cys Tyr Ala Gly Asn Gly Glu Ser Tyr Arg Gly Thr Ala Ser
1 5 10 15

Thr Thr Lys Ser Gly Lys Pro Cys Gln Arg Trp Asp Ser Gln Thr Pro
20 25 30

His Leu His Arg Phe Thr Pro Glu Arg Phe Pro Glu Leu Gly Leu Glu
35 40 45

His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ser Glu Gly Pro Trp Cys
 50 55 60

Tyr Thr Thr Asp Pro Asn Val Arg Trp Glu Tyr Cys Asp Ile Pro Gln
 65 70 75 80

Cys Glu Ser

<210> 87

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like
 serine protease Consensus Sequence

<400> 87

Arg Ile Val Gly Gly Ser Glu Ala Asn Ile Gly Ser Phe Pro Trp Gln
 1 5 10 15

Val Ser Leu Gln Tyr Arg Gly Gly Arg His Phe Cys Gly Gly Ser Leu
 20 25 30

Ile Ser Pro Arg Trp Val Leu Thr Ala Ala His Cys Val Tyr Gly Ser
 35 40 45

Ala Pro Ser Ser Ile Arg Val Arg Leu Gly Ser His Asp Leu Ser Ser
 50 55 60

Gly Glu Glu Thr Gln Thr Val Lys Val Ser Lys Val Ile Val His Pro
 65 70 75 80

Asn Tyr Asn Pro Ser Thr Tyr Asp Asn Asp Ile Ala Leu Leu Lys Leu
 85 90 95

Ser Glu Pro Val Thr Leu Ser Asp Thr Val Arg Pro Ile Cys Leu Pro
 100 105 110

Ser Ser Gly Tyr Asn Val Pro Ala Gly Thr Thr Cys Thr Val Ser Gly
 115 120 125

Trp Gly Arg Thr Ser Glu Ser Ser Gly Ser Leu Pro Asp Thr Leu Gln
 130 135 140

Glu Val Asn Val Pro Ile Val Ser Asn Ala Thr Cys Arg Arg Ala Tyr
 145 150 155 160

Ser Gly Gly Pro Ala Ile Thr Asp Asn Met Leu Cys Ala Gly Gly Leu
 165 170 175

Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
 180 185 190

Cys Asn Asp Pro Arg Trp Val Leu Val Gly Ile Val Ser Trp Gly Ser
 195 200 205

Tyr Gly Cys Ala Arg Pro Asn Lys Pro Gly Val Tyr Thr Arg Val Ser
 210 215 220

Ser Tyr Leu Asp Trp Ile
 225 230

<210> 88

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin
 Consensus Sequence

<400> 88

Ile Val Gly Gly Arg Glu Ala Gln Ala Gly Ser Phe Pro Trp Gln Val
 1 5 10 15

Ser Leu Gln Val Ser Ser Gly His Phe Cys Gly Gly Ser Leu Ile Ser
 20 25 30

Glu Asn Trp Val Leu Thr Ala Ala His Cys Val Ser Gly Ala Ser Ser
 35 40 45

Val Arg Val Val Leu Gly Glu His Asn Leu Gly Thr Thr Glu Gly Thr
 50 55 60

Glu Gln Lys Phe Asp Val Lys Lys Ile Ile Val His Pro Asn Tyr Asn
 65 70 75 80

Pro Asp Thr Asn Asp Ile Ala Leu Leu Lys Leu Lys Ser Pro Val Thr
 85 90 95

Leu Gly Asp Thr Val Arg Pro Ile Cys Leu Pro Ser Ala Ser Ser Asp
 100 105 110

Leu Pro Val Gly Thr Thr Cys Ser Val Ser Gly Trp Gly Arg Thr Lys
 115 120 125

Asn Leu Gly Thr Ser Asp Thr Leu Gln Glu Val Val Val Pro Ile Val
 130 135 140

Ser Arg Glu Thr Cys Arg Ser Ala Tyr Gly Gly Thr Val Thr Asp Thr
 145 150 155 160

Met Ile Cys Ala Gly Ala Leu Gly Gly Lys Asp Ala Cys Gln Gly Asp
 165 170 175

Ser Gly Gly Pro Leu Val Cys Ser Asp Gly Glu Leu Val Gly Ile Val
 180 185 190

Ser Trp Gly Tyr Gly Cys Ala Val Gly Asn Tyr Pro Gly Val Tyr Thr

195 200 205

Arg Val Ser Arg Tyr Leu Asp Trp Ile
210 215

<210> 89
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Divergent
subfamily of APPLE domains Consensus Sequence

<400> 89
Lys Ser Asp Asp Cys Phe Val Arg Leu Pro Asn Thr Lys Leu Pro Asp
1 5 10 15
Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln
20 25 30
Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn
35 40 45
Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala
50 55 60
Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile
65 70 75

<210> 90
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Lipocalin/cytosolic fatty-acid binding protein
family Consensus Sequence

<400> 90
Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro
1 5 10 15
Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile
20 25 30
Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys
35 40 45
Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys
50 55 60
Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val
65 70 75 80

Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly
85 90 95

Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro
100 105 110

Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu
115 120 125

Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg
130 135 140

Cys
145

<210> 91

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin
Consensus Sequence

<400> 91

Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His
1 5 10 15

Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg
20 25 30

Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln
35 40 45

Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys
50 55 60

Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln
65 70 75 80

Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala
85 90 95

Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His
100 105 110

Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu
115 120 125

Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe
130 135 140

Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln
145 150 155 160

Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg
 165 170 175
 Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu
 180 185 190
 Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu
 195 200 205
 Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu
 210 215

<210> 92
 <211> 59
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Src homology 3
 domains Consensus Sequence

<400> 92
 Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro
 1 5 10 15
 Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys
 20 25 30
 Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly
 35 40 45
 Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp
 50 55

<210> 93
 <211> 57
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: SH3 domain
 Consensus Sequence

<400> 93
 Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu
 1 5 10 15
 Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp
 20 25 30
 Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu
 35 40 45
 Ile Pro Ser Asn Tyr Val Glu Pro Val
 50 55

<210> 94
 <211> 91
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fes/CIP4
 homology domain Consensus Sequence

<400> 94
 Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser
 1 5 10 15
 Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met
 20 25 30
 Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys
 35 40 45
 Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly
 50 55 60
 Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu
 65 70 75 80
 Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu
 85 90

<210> 95
 <211> 94
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fes/CIP4
 homology domain Consensus Sequence

<400> 95
 Met Gly Phe Gly Ser Glu Leu Cys Pro Glu Gly His Lys Ala Leu Leu
 1 5 10 15
 Ser Arg Gln Asp Asn Glu Leu Arg Leu Leu Glu Glu Met Lys Lys Phe
 20 25 30
 Met Ala Glu Arg Ala Lys Ile Glu Lys Glu Tyr Ala Gly Lys Leu Gln
 35 40 45
 His Leu Ser Ala Gln Val Gly Lys Gly Pro Ala Thr Ala Glu Gly Glu
 50 55 60
 Asp Glu Leu Ser Ser Leu Lys Ser Trp Ala Val Ile Leu Ser Glu Thr
 65 70 75 80
 Glu Gln Gln Ser Lys Ile His Leu Gln Ile Ser Glu Asp Leu

<220>
<223> Description of Artificial Sequence: Trypsin-like
serine protease Consensus Sequence

Ser Tyr Leu Asp Trp Ile
225 230

<210> 97
 <211> 217
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Trypsin
 Consensus Sequence

<400> 97

Ile	Val	Gly	Gly	Arg	Glu	Ala	Gln	Ala	Gly	Ser	Phe	Pro	Trp	Gln	Val	1	5	10	15
Ser	Leu	Gln	Val	Ser	Ser	Gly	His	Phe	Cys	Gly	Gly	Ser	Leu	Ile	Ser	20	25	30	
Glu	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Val	Ser	Gly	Ala	Ser	Ser	35	40	45	
Val	Arg	Val	Val	Leu	Gly	Glu	His	Asn	Leu	Gly	Thr	Thr	Glu	Gly	Thr	50	55	60	
Glu	Gln	Lys	Phe	Asp	Val	Lys	Lys	Ile	Ile	Val	His	Pro	Asn	Tyr	Asn	65	70	75	80
Pro	Asp	Thr	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Leu	Lys	Ser	Pro	Val	Thr	85	90	95	
Leu	Gly	Asp	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro	Ser	Ala	Ser	Ser	Asp	100	105	110	
Leu	Pro	Val	Gly	Thr	Thr	Cys	Ser	Val	Ser	Gly	Trp	Gly	Arg	Thr	Lys	115	120	125	
Asn	Leu	Gly	Thr	Ser	Asp	Thr	Leu	Gln	Glu	Val	Val	Val	Pro	Ile	Val	130	135	140	
Ser	Arg	Glu	Thr	Cys	Arg	Ser	Ala	Tyr	Gly	Gly	Thr	Val	Thr	Asp	Thr	145	150	155	160
Met	Ile	Cys	Ala	Gly	Ala	Leu	Gly	Gly	Lys	Asp	Ala	Cys	Gln	Gly	Asp	165	170	175	
Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Asp	Gly	Glu	Leu	Val	Gly	Ile	Val	180	185	190	
Ser	Trp	Gly	Tyr	Gly	Cys	Ala	Val	Gly	Asn	Tyr	Pro	Gly	Val	Tyr	Thr	195	200	205	
Arg	Val	Ser	Arg	Tyr	Leu	Asp	Trp	Ile								210	215		

<210> 98
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV5 Primer 1

 <400> 98
 ctcccactcc tgctgcttct gact 24

 <210> 99
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV5 Primer 2

 <400> 99
 aaggctgggc ctaaccacgt ctcat 25

 <210> 100
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV7 Primer 1

 <400> 100
 catgaactgg gcatttctgc agg 23

 <210> 101
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV7 Primer 2

 <400> 101
 ttatctgctg atctcgcagg ttatgga 27

 <210> 102
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 1

 <400> 102
 ctgacaggcc ctggtgtgtg at 22

<210> 103
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV8 Primer 2

 <400> 103
 tcacacatgt ttcatgtggg agttaga 27

 <210> 104
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 1

 <400> 104
 gaggtagagg tcggacagac tgtg 24

 <210> 105
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV9 Primer 2

 <400> 105
 actcatgcaa cttgcttctc tcactct 27

 <210> 106
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV10b Primer
 1

 <400> 106
 cctatgagcc tgatgctgga tgac 24

 <210> 107
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: NOV10b Primer

<400> 107
aggactcaga ggagggagtc ctgag 25

<210> 108
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Forward

<400> 108
gcactacaag tggaagcctt ac 22

<210> 109
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 109
ctcaagtaga agccgactta tgcaaa 26

<210> 110
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag4164 Reverse

<400> 110
tcaaatecctt ctgcgataca gt 22

<210> 111
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ag1313b
Forward

<400> 111
cagctgcacg attaatagaag at 22

<210> 112
<211> 25

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b Probe

 <400> 112
 aggtcttgga ctggccttca ccatt 25

 <210> 113
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse

 <400> 113
 ccaaagttgt gtccagactc at 22

 <210> 114
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2197 Forward

 <400> 114
 ccaaggaaga cctcttcatc tt 22

 <210> 115
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2197 Probe

 <400> 115
 tcttgcttac ggcataagcg ctctct 26

 <210> 116
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2197 Reverse

 <400> 116
 ttcatttcta tgggacctca ga 22

<210> 117
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Forward

 <400> 117
 aaagatggga ctggtcatga c 21

 <210> 118
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Probe

 <400> 118
 cagccatct tactgactgg tctgga 26

 <210> 119
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Reverse

 <400> 119
 gtgcaaatcc caaagtgtca 20

 <210> 120
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Forward

 <400> 120
 gcactacaag tggaagcctt ac 22

 <210> 121
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag4164 Probe

<400> 121
 ctcaagtaga agccgactta tgcaaa 26

<210> 122
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag4164 Reverse

<400> 122
 tcaaatcctt ctgcgatata gt 22

<210> 123
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Forward

<400> 123
 ccaaggaaga cctcttcatc tt 22

<210> 124
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Probe

<400> 124
 tcttgcttac ggcataagcg ctctct 26

<210> 125
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Reverse

<400> 125
 ttcatttcta tgggacctca ga 22

<210> 126
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Forward

<400> 126
 ccaaggaaga cctcttcatc tt 22

<210> 127
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Probe

<400> 127
 tcttgcttac ggcataagcg ctctct 26

<210> 128
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2197 Reverse

<400> 128
 ttcatttcta tgggacctca ga 22

<210> 129
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag708 Forward

<400> 129
 aaagatggga ctcgatcatga c 21

<210> 130
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag708 Probe

<400> 130
 cacgcatct tactgactgg tctgga 26

<210> 131

<211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag708 Reverse

 <400> 131
 gtgcaaattcc caaagtgatca 20

 <210> 132
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Forward

 <400> 132
 cagctgcacg attaatgaag at 22

 <210> 133
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b Probe

 <400> 133
 aggtcttgga ctggccttca ccatt 25

 <210> 134
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1313b
 Reverse

 <400> 134
 ccaaagttgt gtccagactc at 22

 <210> 135
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1537 Forward

<400> 135
 tttcaagaca ccctgtgata cc 22

<210> 136
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1537 Probe

<400> 136
 acttcgtgtc ctgaatgttc caggct 26

<210> 137
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1537 Reverse

<400> 137
 cagaggaatg aaggcataga tg 22

<210> 138
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2432 Forward

<400> 138
 gtaggcaaag ggactcactg t 21

<210> 139
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2432 Probe

<400> 139
 cagaaatcaa taatctttga ctgccg 26

<210> 140
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2432 Reverse

 <400> 140
 gcacattacg tggctgaga 19

 <210> 141
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1250 Forward

 <400> 141
 cgtggtgaac tctgccttat at 22

 <210> 142
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1250 Probe

 <400> 142
 cacagagctg tcgtctttga ccgatt 26

 <210> 143
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag1250 Reverse

 <400> 143
 agtcccctttg cctaccacaa t 21

 <210> 144
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3086 Forward

 <400> 144
 ggacccatt cgactactgt 20

 <210> 145
 <211> 23

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3086 Probe

 <400> 145
 ctgatgacca gccgccatca atc 23

 <210> 146
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3086 Reverse

 <400> 146
 ttctcaaact gcacctggtc 20

 <210> 147
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Forward

 <400> 147
 tctggacgac aactattgcc 20

 <210> 148
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Probe

 <400> 148
 atggtgctac actacggatc cgacg 25

 <210> 149
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag3797 Reverse

 <400> 149
 gtcacagaat tctcgctcga 20

<210> 150
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Forward

 <400> 150
 tatcatcact tgtgatggca aa 22

 <210> 151
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Probe

 <400> 151
 aaaaccgaga gcactttgaa aacaca 26

 <210> 152
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2439 Reverse

 <400> 152
 aaacttctct cccagggtac aa 22

 <210> 153
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Forward

 <400> 153
 tgaacagaac tatgcgaaac aa 22

 <210> 154
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Ag2771 Probe

<400> 154
 tctgggtaag aagtactgcc ccaaacg 27

<210> 155
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag2771 Reverse

<400> 155
 ggctcttcat ctttggatga a 21

<210> 156
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1674 Forward

<400> 156
 ctcactcacc acaaggaggt aa 22

<210> 157
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1674 Probe

<400> 157
 tgacatcaaa ctcaacagtt cccagga 27

<210> 158
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Ag1674 Reverse

<400> 158
 gtctaggaga gagctgagca aa 22

<210> 159
 <211> 78
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PAN domain
Consensus Sequence

<400> 159

Cys Ser Ser Phe Val Arg Val Pro Gly Arg Ser Leu Ser Gly Asn Asp
1 5 10 15

Ile Ser Val Val Asn Val Pro Ser Leu Glu Glu Cys Ala Ala Leu Cys
20 25 30

Leu Glu Glu Pro Arg Val Cys Arg Ser Phe Thr Tyr Asn Asn Lys Ser
35 40 45

Lys Gln Cys Leu Leu Lys Ser Glu Ser Ser Gly Ser Leu Pro Arg Leu
50 55 60

Lys Arg Pro Ser Gln Lys Val Asp Tyr Tyr Glu Lys Ser Cys
65 70 75

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Connexin
homologues Consensus Sequence

<400> 160

Ser Val Trp Gly Asp Glu Gln Ser Asp Phe Thr Cys Asn Thr Gln Gln
1 5 10 15

Pro Gly Cys Glu Asn Val Cys Tyr Asp Gln Phe Phe Pro Ile Ser His
20 25 30

Val Arg

<210> 161

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 161

Asn Glu Gln Lys
1

<210> 162

<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

<400> 162

Asn His Gln Lys
1

<210> 163
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

<400> 163

Asn Asp Glu Gln
1

<210> 164
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

<400> 164

Gln His Arg Lys
1

<210> 165
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

<400> 165

Met Ile Leu Val
1

<210> 166

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

<400> 166

Met Ile Leu Phe

1